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OM nucleic - nucleic search, using sw model

Run on: February 4, 2005, 11:57:46 ; Search time 4373 Seconds

(Without alignments)  
10604.080 Million cell updates/sec

Title: US-10-628-464-1

Perfect score: 957  
Sequence: 1 atgaatgagagaccacatgct.....caagctgtgagacacttga 957

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:\*  
1: gb\_ba:\*  
2: gb\_hhg:\*  
3: gb\_in:\*  
4: gb\_cm:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sts:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vt:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	956.6	100.0	957	6	CQ738424 Sequence
2	956.6	100.0	957	6	CQ800046 Sequence
3	956.6	100.0	957	9	AY114094 Homo sapi
4	956.6	100.0	957	9	AY724955 Homo sapi
5	956.6	100.0	72045	9	AC092214 Homo sapi
6	953.6	99.6	954	6	BD171274 Novel G-P
7	953.6	99.6	954	6	BD185566 Novel G-P
8	941.8	98.4	957	9	AY724866 Pan panis
9	940.6	98.3	957	9	AY724901 Pan trogl
10	932.2	97.4	957	9	AY724923 Gorilla g
11	892.6	93.3	957	9	AY724986 Pongo pyg
12	875	91.4	957	9	AY725022 Macaca mu
13	524.6	54.8	203639	2	AC117625 Mus muscu
14	514.6	53.8	966	10	AF532786 Mus muscu
15	507	53.0	218921	2	AC097912 Rattus no
16	498.6	52.1	966	10	AY362748 Rattus no
17	296	30.9	131565	2	AC143122 Macaca mu
18	249.8	26.1	924	6	BD144615 Novel G-P
19	249.8	26.1	924	6	CQ738419 Sequence

20	249.8	26.1	924	9	AY114093 Homo sapi
21	249.8	26.1	1324	6	AX647249 Sequence
22	249.8	26.1	175228	2	AC143343 Homo sapi
23	249.8	26.1	200123	9	AC073264 Homo sapi
24	248.2	25.9	924	9	AY724891 Pan trogl
25	246.6	25.8	924	6	CQ800004 Sequence
26	246.6	25.8	924	9	AF494232 Homo sapi
27	246.6	25.8	924	9	AY724956 Homo sapi
28	243.4	25.4	924	9	AY724869 Pan panis
29	241.6	25.1	924	9	AY724987 Pongo pyg
30	239.8	25.2	924	9	AY724933 Gorilla g
31	232.2	24.3	924	9	AY725013 Macaca mu
32	230.2	24.1	924	9	AY724831 Papio ham
33	214.8	22.4	3437	6	AX097850 Sequence
34	192.4	20.1	927	10	AF240768 Rattus no
35	192.4	20.1	1295	6	AX097794 Sequence
36	190.8	19.9	223179	2	AC128080 Rattus no
37	138.6	14.5	885	10	AY362747 Pan panis
38	129	13.5	939	9	AY724864 Pan panis
39	127.4	13.3	939	9	AY724931 Gorilla g
40	127	13.3	939	9	AY724899 Pan trogl
41	125.8	13.1	939	9	AY724964 Homo sapi
42	124.6	13.0	990	10	AY362743 Rattus no
43	124.6	13.0	242701	2	AC102972 Rattus no
44	123.8	12.9	939	9	AY724995 Pongo pyg
45	121.4	12.7	186051	2	EX005324 Mus muscu

#### ALIGNMENTS

RESULT 1	CQ738424	Sequence 24358 from Patent WO02068579.	957 bp	DNA	linear	PAT 03-FEB-2004
LOCUS	CQ738424	Sequence 24358 from Patent WO02068579.				
DEFINITION	CQ738424	Sequence 24358 from Patent WO02068579.				
ACCESSION	CQ738424	Sequence 24358 from Patent WO02068579.				
VERSION	CQ738424.1	GI:42339256				
KEYWORDS						
SOURCE						
ORGANISM						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
FEATURES						
ORIGIN						
Query Match						
Best Local Similarity						
Matches						
1	ATGAATGAGACCAATGATGTTCTAGATCTTGGTGACTGACAAAGGACATCATCTTG	60				
1	ATGAATGAGACCAATGATGTTCTAGATCTTGGTGACTGACAAAGGACATCATCTTG	60				
61	GTTACCAATTTACTCTTTACGCTGTAGCAATGACGCAATGCTTCATCATCTGCT	120				
61	GTTACCAATTTACTCTTTACGCTGTAGCAATGACGCAATGCTTCATCATCTGCT	120				
121	GCTCTGGGCGTGGAGTGGGTCTACGAGAAATGTTGCTTGTGTAATGTTAGTT	180				
121	GCTCTGGGCGTGGAGTGGGTCTACGAGAAATGTTGCTTGTGTAATGTTAGTT	180				
181	AGCTTAGGGGCGTCTGCTTGTCTGACATGATGTGTATGGGTAAACATTTATGTT	240				

Db	1b1	AGCCATGGGGCCTCTCGGCTTCTGTGTGACGTAGTGTAATGGGTAACACCATTTATGTT	240
QY	241	TTCTTGCAATCCGATGGCCTTCCCATACAAACCTGTACTGCAAGTTTCTAGCTTTCCAGTGG	300
Db	241	TTCTTGCAATCCGATGGCCTTCCCATACAAACCTGTACTGCAAGTTTCTAGCTTTCCAGTGG	300
QY	301	GACCTCCGAANTGCGCCACCTTAATGAGTCCTACTGAGGTACAGTGTCTTCAATTTGGTG	360
Db	301	GACCTCCGAANTGCGCCACCTTAATGAGTCCTACTGAGGTACAGTGTCTTCAATTTGGTG	360
QY	361	AAAAATGGTACCTTTCACCCACCCCTGTCTTCTTCTGGCTAAAGCAAGTTGTCTGGGTGG	420
Db	361	AAAAATGGTACCTTTCACCCACCCCTGTCTTCTTCTGGCTAAAGCAAGTTGTCTGGGTGG	420
QY	421	CTACCATGGATGCTCTTTCAGCTCTGTAGGGCTCTCAGCTTCCACCAATTCATTTTTC	480
Db	421	CTACCATGGATGCTCTTTCAGCTCTGTAGGGCTCTCAGCTTCCACCAATTCATTTTTC	480
QY	481	ATAGGCACCCACAGAAATGATACAGAACTATTTAAAGAACATCTACACCTTGGAAATGC	540
Db	481	ATAGGCACCCACAGAAATGATACAGAACTATTTAAAGAACATCTACACCTTGGAAATGC	540
QY	541	ACTGGCGATAGCATACGAGAGTACTGTGAGAAATCTATCTTCTCCCTTAAAAATGATT	600
Db	541	ACTGGCGATAGCATACGAGAGTACTGTGAGAAATCTATCTTCTCCCTTAAAAATGATT	600
QY	601	ACTTGGACAAATGCCACCTGCTGTCTTTTCATTTGCATGATTTTGTCTATCATCTCTG	660
Db	601	ACTTGGACAAATGCCACCTGCTGTCTTTTCATTTGCATGATTTTGTCTATCATCTCTG	660
QY	661	GGAAACACAGGAAGAAAGGCTCTCTTTCACACCTAGAAATTCGAGAACCCAGATGTGAG	720
Db	661	GGAAACACAGGAAGAAAGGCTCTCTTTCACACCTAGAAATTCGAGAACCCAGATGTGAG	720
QY	721	GCACACATAAAGGCTCTGTGGCTCTCCTCTTTTGGCATGCTCTTCATCTCAATATTC	780
Db	721	GCACACATAAAGGCTCTGTGGCTCTCCTCTTTTGGCATGCTCTTCATCTCAATATTC	780
QY	781	CTGTCACTGGTCTTTCAGTGTCTGACAGATATTTTCCACCTTGGACATTTAAATCTGGGTG	840
Db	781	CTGTCACTGGTCTTTCAGTGTCTGACAGATATTTTCCACCTTGGACATTTAAATCTGGGTG	840
QY	841	TGGGAGTACAGTATTTATCTGTGTGTGCACAGATTCACCCATCATCTGCTCTTACGACAC	900
Db	841	TGGGAGTACAGTATTTATCTGTGTGTGCACAGATTCACCCATCATCTGCTCTTACGACAC	900
QY	901	TGCAGGCTGAGAGCTGTGCTGAAGAGTGGYCGTTCTCTCAAGGTGGGACACCTTGA	957
Db	901	TGCAGGCTGAGAGCTGTGCTGAAGAGTGGYCGTTCTCTCAAGGTGGGACACCTTGA	957

RESULT 2

LOCUS CQ800046

DEFINITION Sequence 50 from Patent WO2004029087.

ACCESSION CQ800046

VERSION CQ800046.1

KEYWORDS GI:46848968

SOURCE

ORGANISM

Homio sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

957 bp DNA linear PAT 28-APR-2004

REFERENCE

AUTHORS Bufe,B., Hofmann,T., Krautwurst,D., Kuhn,C. and Meyerhof,W.

TITLE Bitter taste receptors

JOURNAL Patent: WO 2004029087-A 50 08-APR-2004;

DEUTSCHES INSTITUT FÜR ERNÄHRUNGSFORSCHUNG (DE)

location/Qualifiers

1..957

**ORIGIN**

Query Match	100.0%;	Score 956.6;	DB 6;	Length 957;
Best Local Similarity	99.9%;	Pred. No. 3.6e-284;		
Matches 956; Conservative	1;	Mismatches 0;	Indels 0;	Gaps 0;

OY	ATGAATGAGACACCAATGAGTTCTAGAAATCTGGAGTACGACAAAGGCAATCATCTTG	60
Db	1 ATGAATGAGACACCAATGAGTTCTAGAAATCTGGAGTACGACAAAGGCAATCATCTTG	60
OY	61 GTTACCAATTTTACTCTTTTACGCTGGTAGCAATAGGAGCAATGAGCTTATCATCTCT	120
Db	61 GTTACCAATTTTACTCTTTTACGCTGGTAGCAATAGGAGCAATGAGCTTATCATCTCT	120
OY	121 GCTCTGGGCGTGGAGTGGGTGCTAGAGGAATGTTGTTGCTTGTGATTAAGTTATGGTT	180
Db	121 GCTCTGGGCGTGGAGTGGGTGCTAGAGGAATGTTGTTGCTTGTGATTAAGTTATGGTT	180
OY	181 AGCCTAAGGGGCGCTCGCTTCTGTCTGACAGTCAAGGTAAATGAGGTAAGCAATTAATGTT	240
Db	181 AGCCTAAGGGGCGCTCGCTTCTGTCTGACAGTCAAGGTAAATGAGGTAAGCAATTAATGTT	240
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Db	301 GACTTCTGAAATGCTGCCACTTAAATGATCTCTACCTGGCTCAATGCTTCTATATGGTG	360
OY	361 AAAATTGCTACCTTCAACCCACCGCTCTCTCTCTGGCTAAAGACAAGTTGTCTGGGTGG	420
Db	361 AAAATTGCTACCTTCAACCCACCGCTCTCTCTCTGGCTAAAGACAAGTTGTCTGGGTGG	420
OY	421 CTACACATGATGCTCTTACGCTCTGTAGAGGCTCTGCAGCTTCAACACACATTTATTTTTTC	480
Db	421 CTACACATGATGCTCTTACGCTCTGTAGAGGCTCTGCAGCTTCAACACACATTTATTTTTTC	480
OY	481 ATAGGCAACCAAGAAATGATCAGAACTATTAAGAAACATCTACCACTTGGAAATGTC	540
Db	481 ATAGGCAACCAAGAAATGATCAGAACTATTAAGAAACATCTACCACTTGGAAATGTC	540
OY	541 ACTGGCGATGACATCGAGACTACTGTGAGAAATCTATCTCTTCCCTCTAAAAATGATT	600
Db	541 ACTGGCGATGACATCGAGACTACTGTGAGAAATCTATCTCTTCCCTCTAAAAATGATT	600
OY	601 ACTTGGACAATGCCCACCTGCTGCTTTTTCATTTGCAATGATTTTGTCTATCACAATCTCTG	660
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OY	661 GGAAGACACAGGAAGAGGCTCTCTTACAACTCAGAAATTCGAGAGGCCAGTGTCCAG	720
Db	661 GGAAGACACAGGAAGAGGCTCTCTTACAACTCAGAAATTCGAGAGGCCAGTGTCCAG	720
OY	721 GCAACATTAAGGCTGTGCTGGCTCCCTCTCTTTTGGCATGCTCTTCAATCTCATATTTTC	780
Db	721 GCAACATTAAGGCTGTGCTGGCTCCCTCTCTTTTGGCATGCTCTTCAATCTCATATTTTC	780
OY	781 CTGTCACTGTGTTTCAGTGTGCTGCAGGTAATTTTTCACCTCTGACATTTAAATTCGGGTG	840
Db	781 CTGTCACTGTGTTTCAGTGTGCTGCAGGTAATTTTTCACCTCTGACATTTAAATTCGGGTG	840
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Db	841 TGGGAGTCAATGATTTTATCTGTGTGACAGAGTTCAACCCCATCATTTCTGCTTTCAGAAC	900
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Db	901 TGCAGGCTGAGAGCTGTGCTGAAGAGTGGTGGTTCCTCAAGAGTGGGAGCAACCTTGA	957

RESULT 3  
AY114094

LOCUS AY114094 957 bp DNA linear PRI 28-FEB-2003  
DEFINITION Homo sapiens putative taste receptor T2R60 gene, complete cds.  
ACCESSION AY114094  
VERSION AY114094.1 GI:28603637  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
AUTHORS 1 (bases 1 to 957)  
Conte, C., Ebeldin, M., Marcuz, A., Nef, P. and Andres-Barquin, P.J.  
TITLE Identification and characterization of human taste receptor genes  
belonging to the TAS2R family  
JOURNAL Cytogenet. Genome Res. 98 (1), 45-53 (2002)  
MEDLINE 22471936  
PubMed 12584440  
REFERENCE 2 (bases 1 to 957)  
Conte, C., Ebeldin, M., Marcuz, A., Nef, P. and Andres-Barquin, P.J.  
TITLE Direct Submission  
JOURNAL Submitted (17-MAY-2002) Pharma Research Basel, F. Hoffmann-La Roche  
Ltd., Grenzacherstrasse 124, Basel CH-4070, Switzerland  
LOCATION/Qualifiers  
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ORIGIN  
Query Match 100.0%; Score 956.6; DB 9; Length 957;  
Best Local Similarity 99.9%; Pred. No. 3.6e-284;  
Matches 956; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGATGAGAGACACATGTTCTAGATCTTCGGTGACTGACAAGAGCCCATCATCTTG 60  
Db 1 ATGATGAGAGACACATGTTCTAGATCTTCGGTGACTGACAAGAGCCCATCATCTTG 60  
QY 61 GTTACATTTTACTCTTTTACGCTGCTGAGCAATAGCAGCAATGGCTTCATCATGCT 120  
Db 61 GTTACATTTTACTCTTTTACGCTGCTGAGCAATAGCAGCAATGGCTTCATCATGCT 120  
QY 121 GCTCTGGGCGTGGAGTGGGTCTACGAGAGATGTTGGTCCCTTGAGTAAGTATGGTT 180  
Db 121 GCTCTGGGCGTGGAGTGGGTCTACGAGAGATGTTGGTCCCTTGAGTAAGTATGGTT 180  
QY 181 AGCCTAGGGGCGCTCTCGCTTGTCTGTCAGTCACTGATGATGGTAAAGACATTATGTT 240  
Db 181 AGCCTAGGGGCGCTCTCGCTTGTCTGTCAGTCACTGATGATGGTAAAGACATTATGTT 240  
QY 241 TTCTTGCAATCCGATGGCTTCCATPACAACCTGTGACTGCAATTTTCAAGCTTCCAGTGG 300  
Db 241 TTCTTGCAATCCGATGGCTTCCATPACAACCTGTGACTGCAATTTTCAAGCTTCCAGTGG 300  
QY 301 GACTTCCGATGCTGCACCTTATGTCCTCTACCTGGCTCAGTGTCTTATATTTGTTG 360  
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Db 661 GGAAGACACAGAAAGAGCTCTCTTACAACTCAGATTCGAGAGCCAGTGTGACG 720  
QY 721 GCAACATPAAAGCTGCTGCTCTCTCTCTTTTGGCATGCTCTTCAATCTCATATTTTC 780  
Db 721 GCAACATPAAAGCTGCTGCTCTCTCTCTCTTTTGGCATGCTCTTCAATCTCATATTTTC 780  
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Db 781 CTGTCACTGCTGTCTGCTGCTGAGATTTTTCACCTTGAACCTTAAATCTGGGTC 840  
QY 841 TGGAGTCACTGATTTATCTGTGTGAGAGCTGCTGCTCTTCTTCAAGTGTGGACACCTTGA 900  
Db 841 TGGAGTCACTGATTTATCTGTGTGAGAGCTGCTGCTCTTCTTCAAGTGTGGACAC 900  
QY 901 TGGAGTCACTGATTTATCTGTGTGAGAGCTGCTGCTCTTCTTCAAGTGTGGACACCTTGA 957  
Db 901 TGGAGTCACTGATTTATCTGTGTGAGAGCTGCTGCTCTTCTTCAAGTGTGGACAC 957

RESULT 4  
AY724955  
LOCUS AY724955 957 bp DNA linear PRI 18-SEP-2004  
DEFINITION Homo sapiens chromosome 7 taste receptor T2R56 gene, complete cds.  
ACCESSION AY724955  
VERSION AY724955.1 GI:51989208  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
AUTHORS 1 (bases 1 to 957)  
Anne, F., Yoav, G., Orna, M. and Svante, P.  
TITLE Evolution of bitter taste receptors in human and apes  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 957)  
AUTHORS Anne, F., Yoav, G., Orna, M. and Svante, P.  
TITLE Direct Submission  
JOURNAL Submitted (12-NOV-2004) Genetics, Max-Planck Institute for  
Evolutionary Anthropology, Deutscher Platz 6, Leipzig 04103,  
Germany  
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## ORIGIN

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Query Match	Local Similarity	Score	DB %	Length	957
Best Local Similarity	100.0%	956.6	DB 9	Length 957	
Matches	957	Conservative	0	Mismatches	0
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DB	121	GCTCTGGGCGTGAAGTGGTGTACGAGAAATGTTGCTTGTGATTAATGTTG	180		
QY	181	AGCTTGGGGCTCTGCTCTGCTGACATGATGATTAAGGATTAAGACATTAATG	240		
DB	181	AGCTTGGGGCTCTGCTCTGCTGACATGATGATTAAGGATTAAGACATTAATG	240		
QY	241	TTCCTGATCGATGAGGCTTCCATACACCTGTGACATGATTTTCACTTCCAGTG	300		
DB	241	TTCCTGATCGATGAGGCTTCCATACACCTGTGACATGATTTTCACTTCCAGTG	300		
QY	301	GACTTCTGATAGCTGACCTTATGCTCTTCACTGCTGATGTTCTTATTTGTG	360		
DB	301	GACTTCTGATAGCTGACCTTATGCTCTTCACTGCTGATGTTCTTATTTGTG	360		
QY	361	AAATGCTCTCTTCAACCCGCTCTCTGCTGATTAAGGACAAATGTCGGGTG	420		
DB	361	AAATGCTCTCTTCAACCCGCTCTCTGCTGATTAAGGACAAATGTCGGGTG	420		
QY	421	CTACATGATGCTCTTCACTGCTGATGAGGCTCTCAGTTTCAACCATTTTATTTTC	480		
DB	421	CTACATGATGCTCTTCACTGCTGATGAGGCTCTCAGTTTCAACCATTTTATTTTC	480		
QY	481	ATAGGCAACACAGATGATATCAAACTATTAAAGAACATCTACAACTTGGATGTC	540		
DB	481	ATAGGCAACACAGATGATATCAAACTATTAAAGAACATCTACAACTTGGATGTC	540		
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DB	541	ACTGGGATGATGATGAGGATCTGAGAAATTCATCTTCCCTTAAATGATG	600		
QY	601	ACTTGGACATGCGCATGCTCTTCTTTTATTTGATTTGCTCATCATCTCTG	660		
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QY	661	GGAAGACACAGAAAGGCTCTCTTCAAACTCAGAGATCCGAGAGCCAGTGCAG	720		
DB	661	GGAAGACACAGAAAGGCTCTCTTCAAACTCAGAGATCCGAGAGCCAGTGCAG	720		
QY	721	GCAACATAAAGGCTGCTGCTCTCTCTTTTGCATGCTCTTCACTCATTAATTC	780		
DB	721	GCAACATAAAGGCTGCTGCTCTCTCTTTTGCATGCTCTTCACTCATTAATTC	780		
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# RESULT 5 AC092214 LOCUS DEFINITION AC092214 VERSION KEYWORDS SOURCE ORGANISM

## REFERENCE AUTHORS

AC092214 72045 bp DNA linear PRI 31-JAN-2004  
Homo sapiens BAC clone RP11-811J9 from 7, complete sequence.  
AC092214.3 GI:16931065  
HTG.  
Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
1 (bases 1 to 72045)  
Hillier, L.W., Fulton, R.S., Fulton, L.A., Graves, T.A., Pepin, K.H.,  
Wagner, M.C., McPherson, C., Layman, D., Maas, J., Jaeger, S., Walker, R.,  
Wylie, K., Sekhon, M., Becker, M.C., O'Leary, M.D., Schaller, M.E.,  
Fowell, G.A., Delhanty, K.D., Miner, T.L., Nash, M.E., Cordes, M.,  
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Spiele, J., Bieri, T.A., Nelson, J.O., Berkowicz, N., Wohldmann, P.E.,  
Cook, L.L., Hickenbotham, M.T., Eldred, J., Williams, D., Bedell, J.A.,  
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Haugen, E., Gillet, W., Zhou, Y., James, R., Phelps, K., Iadonito, S.,  
Bubb, K., Stamm, B., Levy, R., Glendinning, J., Kaul, R., Kent, W.C.,  
Furey, T.S., Baerbach, R.A., Brent, M.R., Kiebler, E., Flicek, P.,  
Bork, P., Suyama, M., Bailey, J.A., Portnoy, M.E., Torrens, D.,  
Chinwalla, A.T., Gish, W.R., Eddy, S.R., McPherson, J.D., Olson, M.V.,  
Fischer, E.E., Green, E.D., Waterston, R.H., and Wilson, R.K.  
The DNA sequence of human chromosome 7  
Nature 424 (6945), 157-164 (2003)  
22737999  
JOURNAL  
MEDLINE  
PUBMED  
12853948  
2 (bases 1 to 72045)  
Doebber, A., Elliott, G., Kozlowicz, A., and Sun, H.  
The sequence of Homo sapiens BAC clone RP11-811J9  
Unpublished (2001)  
3 (bases 1 to 72045)  
Waterston, R.H.  
Direct Submission  
Submitted (129-JUN-2001) Genome Sequencing Center, Washington  
University School of Medicine, 4444 Forest Park Parkway, St. Louis,  
MO 63108, USA  
4 (bases 1 to 72045)  
Waterston, R.H.  
Direct Submission  
Submitted (15-NOV-2001) Genome Sequencing Center, Washington  
University School of Medicine, 4444 Forest Park Parkway, St. Louis,  
MO 63108, USA  
5 (bases 1 to 72045)  
Waterston, R.H.  
Direct Submission  
Submitted (03-JAN-2002) Genome Sequencing Center, Washington  
University School of Medicine, 4444 Forest Park Parkway, St. Louis,  
MO 63108, USA  
6 (bases 1 to 72045)  
Waterston, R.  
Direct Submission  
Submitted (10-JAN-2002) Department of Genetics, Washington  
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA  
7 (bases 1 to 72045)  
Wilson, R.  
Direct Submission  
Submitted (31-JAN-2004) Department of Genetics, Washington  
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA  
On Nov 15, 2001 this sequence version replaced gi:15625026.  
----- Genome Center  
Center: Washington University Genome Sequencing Center

Center code: WUGSC  
Web site: <http://genome.wustl.edu>  
Contact: [sapiens@wustl.wustl.edu](mailto:sapiens@wustl.wustl.edu)  
----- Summary Statistics -----  
Center project name: H\_NH0811J09

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:  
all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:  
The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 7 Mapping Project (Eric D. Green, Director), John D. McPherson in the Department of Genetics (Washington University), and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see <http://www.nhgri.nih.gov/DIR/GRB/CH7>, send <mailto:egreen@nhgri.nih.gov>, or see <http://genome.wustl.edu>

SOURCE INFORMATION:  
The RPCL-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Moon, P.Y., Zhao, B., Fritngen, R., Tatemio, M., Catanese, J.J., and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. *Genomics* 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at <http://www.chori.org>  
VECTOR: pBACe3.6

NEIGHBORING SEQUENCE INFORMATION:  
The clone sequenced to the left is RP11-563K23 the clone sequenced to the right is RP11-298A10, 2000 bp overlap. Actual start of this clone is at base position 1 of RP11-811J9 actual end is at base position 140619 of RP11-298A10.  
Location/Qualifiers

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DEFINITION	Novel G protein-coupled receptor and its DNA.		
ACCESSION	BD185566		
VERSION	BD185566.1	GI:31877766	
KEYWORDS	JP 2002360279-A/1.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	1 (bases 1 to 954)		
TITLE	Miwa,M., Ito,T., Shintani,Y. and Miyajima,N.		
JOURNAL	Novel G protein-coupled receptor and its DNA Patent: JP 2002360279-A 1 17-DEC-2002; TAKEDA CHEMICAL INDUSTRIES LTD		
COMMENT	OS Homo sapiens (human) PN JP 2002360279-A/1 PD 17-DEC-2002 PF 17-JAN-2002 JP 2002008445 PI MASANORI MIWA,TAKASHI ITO,YASUSHI SHINTANI,NOBUYUKI MIYAJIMA PC C12N15/09,A61K39/395,A61K45/00,A61P1/00,A61P3/00, PC A61P9/00 PC A61P9/00,A61P11/00,A61P25/28,A61P29/00,A61P31/00,A61P35/00, A61P37/00, PC C07K14/705,C07K16/28,C12N1/15,C12N1/19,C12N1/21,C12N5/10, PC C12P21/02, PC C12O1/02,C12Q1/68,G01N33/15,G01N33/50,G01N33/53,G01N33/53, PC G01N33/566', PC C12N15/00,C12N5/00 CC Novel G protein-coupled receptor and its DNA FH Key Location/Qualifiers FT source 1..954 /organism='Homo sapiens (human)'. FT Location/Qualifiers 1..954 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606"		
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ACCESSION			
AY724866.1			
VERSION			
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KEYWORDS			
Pan paniscus (pygmy chimpanzee)			
SOURCE			
Pan paniscus			
ORGANISM			
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Pan.			
REFERENCE			
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TITLE Direct Submission  
JOURNAL Submitted (12-AUG-2004) Genetics, Max-Planck Institute for  
Evolutionary Anthropology, Deutscher Platz 6, Leipzig 04103,  
Germany

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Source Location/Qualifiers

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## ORIGIN

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RESULT 9  
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LOCUS Pan troglodytes chromosome 7 taste receptor T2R56 gene, complete  
DEFINITION  
ACCESSION  
AY724901  
VERSION  
AY724901.1 GI:51989117  
KEYWORDS  
SOURCE  
ORGANISM  
Pan troglodytes (chimpanzee)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Pan.  
REFERENCE  
1 (bases 1 to 957)  
Anne, F., Yoav, G., Orna, M. and Svante, P.  
Evolution of bitter taste receptors in human and apes  
JOURNAL  
TITLE  
Evolution of bitter taste receptors in human and apes  
AUTHORS  
Anne, F., Yoav, G., Orna, M. and Svante, P.  
DIRECT SUBMISSION  
SUBMITTED (12-AUG-2004) Genetics, Max-Planck Institute for  
Evolutionary Anthropology, Deutscher Platz 6, Leipzig 04103,  
Germany

## FEATURES

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## ORIGIN

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121 GCTCTGGCGCTGAGAGTGGTCTACGAGAAATGTTGCTGCTGTGATTAAGTTATGGTT 180



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RESULT	10
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DEFINITION	AJ724923 957 bp DNA linear PRI 18-SEP-2004 Gorilla gorilla chromosome 7 taste receptor TRS6 gene, complete cds.
ACCESSION	AJ724923
VERSION	AJ724923.1 GI:5189154
KEYWORDS	.
SOURCE	Gorilla gorilla (gorilla)
ORGANISM	Gorilla gorilla
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Gorilla. 1 (bases 1 to 957) Anne F., Yoav G., Orna M. and Svante P. Evolution of bitter taste receptors in human and apes Unpublished 2 (bases 1 to 957)
TITLE	
JOURNAL	
REFERENCE	

**AUTHORS** Anne, F., Yoav, G., Orna, M. and Svante, P.  
**TITLE** Direct Submission  
**JOURNAL** Submitted (12-ANG-2004) Genetics, Max-Planck Institute for  
Evolutionary Anthropology, Deutscher Platz 6, Leipzig 04103  
Germany  
**Location/Email**

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**CDS**

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VERSION AY724986.1 GI:51989260  
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SOURCE Pongo pygmaeus (orangutan)  
ORGANISM Pongo pygmaeus  
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Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Pongo.

REFERENCE 1 (bases 1 to 957)  
Anne, F., Yoav, G., Orna, M. and Svante, P.  
Evolution of bitter taste receptors in human and apes  
Unpublished 2 (bases 1 to 957)  
JOURNAL  
AUTHORS Anne, F., Yoav, G., Orna, M. and Svante, P.  
REFERENCE Direct Submission  
AUTHORS Submitted (12-AUG-2004) Genetica, Max-Planck Institute for  
JOURNAL Evolutionary Anthropology, Deutscher Platz 6, Leipzig 04103,  
Germany

FEATURES  
source Location/Qualifiers

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DEFINITION cds.  
ACCESSION AY725022  
VERSION AY725022.1 GI:51989321  
KEYWORDS  
SOURCE Macaca mulatta (rhesus monkey)  
ORGANISM Macaca mulatta  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Macaca.  
REFERENCE 1 (bases 1 to 957)  
Anne, F., Yoav, G., Orna, M. and Svante, P.  
Evolution of bitter taste receptors in human and apes



Kamat, A., Karacas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, X., Lui, A., Mabbitt, R., Maclean, C., Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Meldrum, J., Menus, L., Mihova, T., Mienge, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phukhang, P., Pierre, N., Raghupathi, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schuback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Talamas, J., Testave, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Venkataraman, V., S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Submitted (13-MAR-2004) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA  
On Mar 13, 2004 this sequence version replaced gi:37591301.  
All repeats were identified using RepeatMasker:  
Smith, A.P.A. & Green, P. (1996-1997)  
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

Center: Whitehead Institute/ MIT Center for Genome Research  
Center code: WIBR  
Web site: <http://www-seq.wi.mit.edu>  
Contact: [sequence\\_submissions@genome.wi.mit.edu](mailto:sequence_submissions@genome.wi.mit.edu)  
Project Information  
Center project name: L23370  
Center clone name: 115 M.13

----- Summary Statistics -----  
Sequencing vector: Plasmid; n/a; 100% of reads  
Chemistry: Dye-terminator Big Dye; 100% of reads  
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Insert size: 203825; sum-of-coverage  
Quality coverage: 10.9 in Q20 bases; agarose-fp  
Quality coverage: 10.6 in Q20 bases; sum-of-coverage

\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 6 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

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CC The present sequence encodes human bitter taste receptor T2R76. The human  
CC T2R76 gene is located on chromosome 7 in the region 14q62q92-14q63q48.  
CC The reading frame of T2R76 is intronless. T2R76 polypeptides and  
CC polynucleotides are useful for identifying modulators. Such modulators  
CC are useful for modulating bitter taste perception in a subject. T2R76  
CC agonists can be administered to enhance bitter tastes, while T2R76  
CC antagonists can be administered to reduce bitter tastes.

XX Sequence 957 BP; 203 A; 241 C; 215 G; 298 T; 0 U; 0 Other;

Query Match 100.0%; Score 956.6; DB 12; Length 957;  
Best Local Similarity 99.9%; Pred. NO. 1.8e-292;

Matches 956; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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DB 241 TTCTTGATCCGATGGCTTCCCAATACACCTGTGATCTGACATGTTTCAAGTTCAGTGG 300
QY 301 GACTTCCTGAATGTGCGACCTTATGGTCCCTACCGGCGTCAAGTGTCTTATTTG 360
DB 301 GACTTCCTGAATGTGCGACCTTATGGTCCCTACCGGCGTCAAGTGTCTTATTTG 360
QY 361 AAAATGTCTACCTTCAACCAACCCCTGCTTCTTGCTGTAAGAACAAGTGTGAGTGG 420
DB 361 AAAATGTCTACCTTCAACCAACCCCTGCTTCTTGCTGTAAGAACAAGTGTGAGTGG 420
QY 421 CTACCATGATGCTCTTCAAGCTCTGTAGGGCTCTCCAGCTTCAACCACTTATTTTTC 480
DB 421 CTACCATGATGCTCTTCAAGCTCTGTAGGGCTCTCCAGCTTCAACCACTTATTTTTC 480
QY 481 ATAGGCAACCAAGAAATGATCAAACTATTTAAGAAACATCTACAACCTTGAATGTC 540
DB 481 ATAGGCAACCAAGAAATGATCAAACTATTTAAGAAACATCTACAACCTTGAATGTC 540
QY 541 ACTGGCGATGACATACGAGACTACTGTGAGAAATTCATCTCTTCCCTCTAAAAATGATT 600
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QY 661 GGAAGACACAGGAAGAAAGGCTCTCTTACAACCTCAAGAAATCCGAGAGCCCAATGTGAG 720
DB 661 GGAAGACACAGGAAGAAAGGCTCTCTTACAACCTCAAGAAATCCGAGAGCCCAATGTGAG 720
QY 721 GCACACATAAAGGCTGCTGCTCTCTCTCTTTTGGCAGTGTCTTCATCTCATATTTTC 780
DB 721 GCACACATAAAGGCTGCTGCTCTCTCTCTCTTTTGGCAGTGTCTTCATCTCATATTTTC 780
QY 781 CTGTCACTGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840
DB 781 CTGTCACTGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840
QY 841 TGGGAGTCACTGATTTATCTGTGTGAGAGCTTCAACCCCATCTTGTCTTCAAGAAC 900
DB 841 TGGGAGTCACTGATTTATCTGTGTGAGAGCTTCAACCCCATCTTGTCTTCAAGAAC 900
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QY 901 TGCAGGCTGAGAGCTGTGCTGAGAGTCTGCTTCTCAAGGTGTGGACACCTTGA 957  
DB 901 TGCAGGCTGAGAGCTGTGCTGAGAGTCTGCTTCTCAAGGTGTGGACACCTTGA 957

## RESULT 2

ADM3336  
ADM3336 standard; cDNA; 957 BP.

XX ADM3336;

DT 18-NOV-2004 (first entry)

DE Human bitter taste receptor TAS2R60 encoding cDNA SEQ ID NO:50.

XX human; bitter taste receptor; food; gene; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

FT CDS 1..957 /tag= a /product= "bitter taste receptor hTAS2R60"

XX MO2004029087-A2.

XX 08-APR-2004.

XX 25-SEP-2003; 2003MO-BE010691.

XX 25-SEP-2002; 2002US-0413298P.

XX (DEER-) DEUT INST ERNAERUNGSPORSCHUNG POTSDAM.

XX Bufo B, Hofmann T, Krautwurst D, Kuhn C, Meyernhof W;

XX WPI; 2004-305149/28.

XX P-PSDB; ADM3335.

XX Novel bitter receptor polynucleotide encoding human TAS2R protein having

XX bitter substance binding activity, useful for producing nutraceutical or

XX pharmaceutical compositions comprising antagonists of bitter taste

XX receptor activity.

XX Claim 14; SEQ ID NO 50; 108bp; English.

XX The present sequence encodes a human bitter taste receptor. Also

XX described: (1) a polynucleotide encoding a bitter taste receptor (I); (2)

XX a vector (II) containing (I); (3) a host cell (III) genetically

XX engineered with (I) or (II); (4) a transgenic non-human animal (IV)

XX containing (I), (II) and/or (III); (5) a polypeptide (V) having the amino

XX acid sequence encoded by (I) or obtained by culturing (III) and

XX recovering polypeptide; (6) an antibody (VI) specifically binding to (V);

XX (7) a nucleic acid molecule (VII) specifically hybridizing to (I); (8) an

XX antagonist/inhibitor (VIII) against (V) which is antibody, the

XX extracellular domain of (V) or its fragment or an inhibiting RNA; (9)

XX isolating (M1) a compound that binds to (V) encoded by (I); (10)

XX isolating (M2) an antagonist of bitter taste receptor activity; (11) a

XX foodstuff including human and animal foodstuff, any precursor material or

XX additive employed in the production of foodstuff comprising (VIII); and

XX (12) a nutraceutical/pharmaceutical composition comprising (VIII) and an

XX active agent and optionally a carrier. (III) is useful for producing a

XX polypeptide encoded by (I), which involves culturing (III) and recovering

XX the polypeptide encoded by (I). (II) is useful for producing cells

XX capable of expressing at least one of the bitter taste receptor

XX polypeptide, which involves genetically cells in vitro with (I), where

XX the bitter taste receptor polypeptide(s) is/are encoded by (I). (M1) or

XX (M2) can be used for producing food or any precursor material or additive

XX employed in the production of foodstuffs. (M1) or (M2) can also be used

XX for producing nutraceutical or pharmaceutical compositions. (I), (II),

XX (VI) or (VIII) can be used for manufacturing a medicament for the

XX treatment of an abnormally increased or decreased sensitivity towards a

CC bitter substance. The identified agonist/inhibitor efficiently suppresses  
CC or eliminated bitter tasting components of food and effectively useful in  
CC food industries.

XX Sequence 957 BP; 203 A; 240 C; 215 G; 299 T; 0 U; 0 Other;

Query Match 100.0%; Score 956.6; DB 13; Length 957;  
Best Local Similarity 99.9%; Pred. No. 1.8e-292;  
Matches 956; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ATGATGAGAGACCATGTTCTAGATCTTGGTGACTGACAGAAAGGCGCATCTTG 60
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DB 61 GTTACCACTTTTACTCTTTTACGCTTGTAGCAATACAGGCAATGCTTCATCAGCT 120
QY 121 GCTTGGGCGGTGAGTGGGCTGACGAGAAATGTTGGCTTGTGATTAAGTTATGGTT 180
DB 121 GCTTGGGCGGTGAGTGGGCTGACGAGAAATGTTGGCTTGTGATTAAGTTATGGTT 180
QY 181 AGCCTAGGGGCTCTCCCTCTGTCTGACAGTCACTGTAATGGGTAAAGACCATTTATGT 240
DB 181 AGCCTAGGGGCTCTCCCTCTGTCTGACAGTCACTGTAATGGGTAAAGACCATTTATGT 240
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DB 241 TTCTTGATCCGATGCGCTTCCCATPACACCTGTACTGCACTTTTCACTTCACTGG 300
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QY 481 ATGAGCAACCAACAATGTAATCAGATCTTAAAGAACATCTAACACCTTGAATGTC 540
DB 481 ATGAGCAACCAACAATGTAATCAGATCTTAAAGAACATCTAACACCTTGAATGTC 540
QY 541 ACTGCGATAGCATACGAGAGCTACTGTGAGAAATTTATCTTCCCTTAAATGATT 600
DB 541 ACTGCGATAGCATACGAGAGCTACTGTGAGAAATTTATCTTCCCTTAAATGATT 600
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DB 721 GCACACATTAAGGCTGCTGCTCTCTCTCTCTTTTGGCATGCTCTTCACTCAATTTTC 780
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DB 781 CTGTCACTGCTGTCACTGCTGCAAGGTATTTTTCACACTTGTGACTTTAAATTCGGGTG 840
QY 841 TGGAGACAGATGATTTATCTGTGTCAGAGATTTACCCCATCATTTGCTCTTACGACAC 900
DB 841 TGGAGACAGATGATTTATCTGTGTCAGAGATTTACCCCATCATTTGCTCTTACGACAC 900
QY 901 TGCAGGCTGAGAGCTGTGCTGAAGAGTGTCTTCTCAAGTGTGGGACACCTTGA 957
DB 901 TGCAGGCTGAGAGCTGTGCTGAAGAGTGTCTTCTCAAGTGTGGGACACCTTGA 957

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## RESULT 3

ABK87584

ID ABK87584 standard; cDNA; 954 BP.

AC ABK87584;

DT 24-SEP-2002 (first entry)

XX DNA encoding novel human G-protein coupled receptor.

XX G-protein coupled; receptor; liver; central nervous system disease;  
XX Alzheimer's disease; anorexia; dementia; metabolic disease; diabetes;  
XX hyperlipemia; cancer; non-small cell lung cancer; ovarian cancer;  
XX stomach cancer; breast cancer; colon cancer; bladder cancer; rheumatism;  
XX circulatory disease; hypertension; atherosclerosis; angina; allergy;  
XX inflammatory disease; respiratory disease; asthma; bronchitis;  
XX digestive disease; stomach ulcer; duodenal ulcer; immune disorder;  
XX autoimmune disease; infection; acquired immunodeficiency syndrome; AIDS;  
XX pneumonia; influenza; gene; 95.

XX Homo sapiens.

XX Key Location/Qualifiers

XX CDS

FT 1..954  
FT /\*tag= a  
FT /product= "Novel G-protein coupled receptor"  
FT /partial  
FT /note= "No stop codon given"

XX W0200257309-A1.

XX 25-JUL-2002.

XX 17-JAN-2002; 2002MO-JP000271.

XX 18-JAN-2001; 2001JP-00010814.

XX 30-MAR-2001; 2001JP-00102558.

XX (TAKE ) TAKEDA CHEM IND LTD.

XX Miwa M, Ito T, Shintani Y, Miyajima N;

XX WPI; 2002-538457/57.

XX DR P-PSDB; AAU98514.

XX New G-protein coupled receptor protein expressed in human liver for  
XX design of drugs and reagents for treatment and diagnosis of cancer and  
XX respiratory metabolic and other diseases.

XX Claim 6; Page 91; 101pp; Japanese.

XX The invention describes a novel G-protein coupled receptor protein  
XX expressed in human liver. The protein is used in the treatment,  
XX prevention and diagnosis of central nervous system diseases (such as  
XX Alzheimer's, anorexia and dementia), metabolic diseases (such as diabetes  
XX and hyperlipemia), cancer (such as non-small cell lung cancer, ovarian  
XX cancer, stomach cancer, breast cancer, colon cancer and bladder cancer),  
XX circulatory diseases (such as hypertension, atherosclerosis and angina),  
XX inflammatory diseases (such as allergy and rheumatism), respiratory  
XX diseases (such as asthma and bronchitis), digestive diseases (such as  
XX stomach ulcer and duodenal ulcer), immune disorders (such as autoimmune  
XX diseases), and infections (such as acquired immunodeficiency syndrome  
XX (AIDS), pneumonia and influenza). This sequence encodes the novel G-  
XX protein coupled receptor protein described in the invention

XX Sequence 954 BP; 202 A; 241 C; 214 G; 297 T; 0 U; 0 Other;

Query Match 99.6%; Score 953.6; DB 6; Length 954;  
Best Local Similarity 99.9%; Pred. No. 1.6e-291;  
Matches 953; Conservative 1; Mismatches 0; Indels 0; Gaps 0;







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Db      8280 CTGGTTAGTGGCCCAAGCTGATCAAGGGCTCCGATGATCATGTGGCTGGAATCATCT 8339
Qy      473 TATTTCATATGGCAACACAGAAATGATCAGAACTATTAAAGAACCATCTACACCTT 532
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Qy      533 GGAATGTCACCTGGGATGAGCATAGGAGCTCTGAGAAATTTATCTCTCCCTCA 592
Db      8400 ACGAACTCTGATTATAGAGTGAAGGCTTATTTAG--CTCTACTTTTCTTTATG 8456
Qy      593 AAATGATTACTTGGACAATGCCACTGCTCTTTTCAATTTGATGATTTTGTCTATCA 652
Db      8457 AAGGTTTGTGTGTCGATCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 8516
Qy      653 CATCTCTGGGAGACACAGAGAAAGGCTCTCTTACACCTCAGATTCGAGAGCCCA 712
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Qy      833 TCTGGGTGTGGAGTCACTGATTTATCTGTGTGACAGAGTTCAACCATCATTTGCTCT 892
Db      8697 ACTGGGCTGTGTAGTCTATCTATGTGCAACATCTGTGCTGACCTTACCGTCTGTGTC 8756
Qy      893 TCAGCACTGAGGCTGAGAGCTGTGCTGAGAGTCTGCT 933
Db      8757 TGAAGAGCCCCAACTGAATAAGAGGCTTGAAGACATGCTT 8797
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## RESULT 2

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US-09-949-016-2342
; Sequence 2342, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 2342
; LENGTH: 876
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-2342
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Query Match      11.8%; Score 113.2; DB 4; Length 876;
Best Local Similarity 49.3%; Pred. No. 3.6e-26;
Matches 431; Conservative 0; Mismatches 413; Indels 30; Gaps 4;
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Qy      53 TCATCTGTTTACCATTTTACTCTCTTTTACGCTGTAGCAATAGCAGCAATGGCTTCA 112
Db      23 TCTTCTTCATGATCATCTATGTGCTGTAGCTTTCACAAATTATGTGACAGAGCCTTAA 82
Qy      113 TCACTGTGCTCTGGGTGTGAGTGGTGTCTAGGAGAAATGTTGGCTTGTGATAGT 172
Db      83 TTGTGTGAGTGTGGGAGAGAAATGGCTGAAATCAGAAAGCTGATGCTGTGGACATGA 142
Qy      173 TATTGTTTACCTTAAAGGGCTCTGCTCTGTCTGTCAGTGTGATGAGGTAAAGCA 232
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Qy      233 TTTATGTTTCTTGATCCGATGAGGCTTCCCATACAACTCTGATCTGCACTTTAGCTT 232
Db      203 TTGCTCTCTATTATTTAATTATGATATGATTTTGGCAAC-----TTAACAA 247
Qy      293 TCCAGTGGGACTTCTGAAATGCTGCCACTTATATGTCCTTACTGCTGATGTCCTTCT 352
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Qy      353 ATTGTGGAATAATTTGCTACCTTCAACCAACCTGCTCTTCTGAGCTTAAAGCAGATTC 412
Db      308 ACTGATCAAGGTCTCTCTTTTACCCATACATCTTCTCTGCTGAGGTGAGAAATTT 367
Qy      413 CTGGGTGCTACCAATGAGTCTCTTCACTCTGTAGGCTCTTCAAGCTTCAACCAATTC 472
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Qy      473 TATTTCATATGCAACCAAGAAATGATATGAAATTAATTAAGAACATCTTACAACTT 532
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Qy      533 GGAATGTCAGTGGGATAGCATACGAGTACTGTGAGAAATTTCTCTCTCTCTCTTAA 592
Db      485 GAAACAGCACTGTATCTGACAAACTGAAATTTTATCA---GTATCACTTCCAGGCTC 541
Qy      593 AAATGATTACTTGGACATGCCCACTGCTCTTTTTCATTTGATGATTTTGTCTATCA 652
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Qy      713 GTGTGAGGACACATTAAGGCTCTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 772
Db      653 GCATGAAGGCACTTACCTGCTGAGTCCCTGAGGCTCTGCTCTATTTATGTGTTACT 712
Qy      773 CATATTTCTGTCACTGCTGTGCTGCTGAGATTTTTCACCTCTGACCTTTAAAT 832
Db      713 CTTACTTTCTAACCATCTACATCACTATTAAGTACTTATTTGATTAAGATGTTGCT 772
Qy      833 TCTGGGTGTGGAGTCACTGATTTATCTGTGTGACAGAGTTCAACCCATCATTTGCTCT 892
Db      773 TATGGGTCTGGAGCTTTTGTCTATGCTTTCAATTTAATGATTCATCTTCACTGATGC 832
Qy      893 TCAGCACTGAGGCTGAGAGCTGTGCTGAGAG 926
Db      833 TGAAGAGCTTACGTTGAATAAGATTTTAAAGG 866
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## RESULT 3

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US-09-949-016-12790
; Sequence 12790, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
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Oy	181	AACCTAAGGGGCCCTTCCTGCTTCTGTCTGCAAGTCAAGTGTAAATGGTAAGAACATTTATGTT	240
Dd	181	AACCTAAGGGGCCCTTCCTGCTTCTGTCTGCAAGTCAAGTGTAAATGGTAAGAACATTTATGTT	240
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Dd	241	TTCCTTGATCCGATGGCCCTTCCCATACAAACCCTGTACTGAGATTTCTAGCTTCCAGTGG	300
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Dd	361	AAAATGTCTACCTTCAACCAACCCCTGTCTTCTTGGCTAAAGACAAGTGTCTGGGTGG	420
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Dd	421	CTACCATGATGCTCTTCAAGCTCTGTAGAGGCTCTCCAGCTTACACCAATTTCTATTTTTTC	480
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Dd	481	ATAGGCAACCAAGAAATGTATCAGAACTATTAAAGSAAACCATCTACAACTTGGAAATGTC	540
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Dd	601	ACTTGGACAATGCCCACTGCTCTTTTTCATTGATGATATTTTGCATCACATCTCTG	660
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Dd	721	GCACACATAAAGGCTCTGCTGCTCTCTCTCTTTTGGCANGTCTTCACTCATATTTTC	780
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Dd	781	CTGTACCTGTGCTTCAAGTCTGAGGATTTTTCACACTGTGACCTTAAATTTCTGGGTG	840
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Dd	841	TGGAGTCAAGTATTTATCTGTGTGTGACAGCATTTACCCCACATCTTGTGCTTCAGAGAAC	900
Oy	901	TGCAGGCTGAGAGCTGTGCTGAAGAGTCGYCTTCTCAAAGGTGTGGAGACCTTGA	957
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 RESULT 2 US-09-825-882-17 ; Sequence 17, Application US/09825882 ; Patent No. US2002009451A1 ; GENERAL INFORMATION: ; APPLICANT: ADLER, JON ELLIOT ; TITLE OF INVENTION: T2R TASTE RECEPTORS AND GENES ENCODING SAME ; FILE REFERENCE: 078003/0279152/RX1 ; CURRENT APPLICATION NUMBER: US/09/825, 882 ; PRIOR FILING DATE: 2001-04-05 ; PRIOR APPLICATION NUMBER: 60/195,532 ; PRIOR FILING DATE: 2000-04-07 ; PRIOR APPLICATION NUMBER: 60/247,014 ; PRIOR FILING DATE: 2000-11-13 ; NUMBER OF SEQ ID NOS: 31			

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; SOFTWARE:PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 924
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-825-882-17

Query Match      26.1%; Score 249.8; DB 9; Length 924;
Best Local Similarity 56.4%; Pred. No. 6,3e-70;
Matches 489; Conservative 0; Mismatches 372; Indels 6; Gaps 1,

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OY 114 CACGCTGCTGTGGGCGTGGATGGGAGTCAACGGAAATGTTGCTTGTGATTAAGTT 173
DB 81 TGTGCTGTGTGGGCAAGGAGATGCTGCAATATGACAGGTGTGCTGCTTGATGAT 140
OY 174 ATTGATTAGCCTTAAGGGGCTCTGCTCTGTCTGTCAGTCAAGTGTAAATGGTAAGACAT 233
DB 141 CCTCATTAAGCTTGGGTGTCTCCGCTCTGCTGCTGCAAGTGTGTGGAGCGGTGCAACATT 200
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DB 201 CTACTACTCTGCCAGAAAGTGTGAGTCTGTGGGGTCTGGCCGACAGTTCTTCACT 260
OY 294 CCAGTGGGACTCTCTGAATGTGTCACCTTAATGTCTCTTCACTGAGCTCACTGTCTTCTA 353
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OY 774 ATATTTTCTCTGACGTGGTTCAGTGTGCAAGTATTTTTCACCTCTGACCTTAAAT 833
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OY 834 CTGGGTGTGGGAGTCAAGTATTAATCTGTGTGACAGAGTTTACCCCATCATTTCTGCTT 893
DB 795 CTGGCAATGGGAAATTCAGATCTACCTGTGATATCTGTCAATCCTTCATCTCATCTT 854
OY 894 CAGCAACTGACGAGCTGAGAGCTGTCT 920
DB 855 CAGCAACTCAAGCTTGAAGCGTGT 881

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OM nucleic - nucleic search, using sw model

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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 66479088

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

EST: \*  
1: gb\_est1.\*  
2: gb\_est2.\*  
3: gb\_hnc.\*  
4: gb\_est3.\*  
5: gb\_est4.\*  
6: gb\_est5.\*  
7: gb\_est6.\*  
8: gb\_g881.\*  
9: gb\_g882.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	92	9.6	717	CF147792	CF147792 AGENCOURT
2	70.6	7.4	528	BH044856	BH044856 RPECI-24-3
3	69	7.2	787	A2739176	A2739176 RPECI-24-1
4	67.8	7.1	866	CN840760	CN840760 AGENCOURT
5	66.2	6.9	718	CF147794	CF147794 AGENCOURT
6	65	6.8	894	AY403664	AY403664 Mus muscu
7	64	6.7	804	CN841612	CN841612 AGENCOURT
8	63.4	6.6	493	B2898478	B2898478 CH240_14L
9	63	6.6	900	AY404526	AY404526 Homo sapi
10	63	6.6	917	CN842886	CN842886 AGENCOURT
11	62.4	6.5	707	CN843127	CN843127 AGENCOURT
12	62.4	6.5	863	CN843111	CN843111 AGENCOURT
13	62.4	6.5	885	CN843127	CN843127 AGENCOURT
14	62.2	6.5	771	CC544773	CC544773 CH240_427
15	61.8	6.5	900	AY404527	AY404527 Pan trogl
16	61.2	6.4	893	AY403663	AY403663 AGENCOURT
17	59.2	6.2	715	CF147795	CF147795 AGENCOURT
18	59	6.2	737	CO960534	CO960534 AGENCOURT
19	58	6.1	650	AQ316999	AQ316999 CITR1-E1-
20	58	6.1	742	AQ308694	AQ308694 CITR1-E1-
21	58	6.1	850	CN835406	CN835406 AGENCOURT
22	58	6.1	895	CN839536	CN839536 AGENCOURT
23	58	6.1	900	AY403662	AY403662 Homo sapi
24	57.6	6.0	744	CO935442	CO935442 AGENCOURT

C	25	57.6	6.0	913	7	CN843081	CN843081 AGENCOURT
C	26	56.8	5.9	790	7	CO959975	CO959975 AGENCOURT
C	27	56.2	5.9	894	9	AY404528	AY404528 Mus muscu
C	28	55.6	5.8	2418	3	AF116728	AF116728 Homo sapi
C	29	54.4	5.7	397	8	AQ164951	AQ164951 HS_3014_B
C	30	53.8	5.6	530	9	CE673154	CE673154 tigr-g8s-
C	31	53.6	5.6	414	4	BH614820	BH614820 UP_535-10
C	32	53.6	5.6	806	4	BG209561	BG209561 RST29087
C	33	53.6	5.6	884	7	CN839562	CN839562 AGENCOURT
C	34	53.2	5.6	851	9	CC521365	CC521365 CH240_369
C	35	52.2	5.5	689	7	CO959518	CO959518 AGENCOURT
C	36	52	5.4	921	7	CN843110	CN843110 AGENCOURT
C	37	51.8	5.4	330	2	AW266498	AW266498 ZG24_gast
C	38	51.8	5.4	758	4	BG203110	BG203110 RST22479
C	39	51.4	5.4	498	8	AO616191	AO616191 HS_5148_A
C	40	51.2	5.4	681	9	CE066229	CE066229 tigr-g8s-
C	41	50.8	5.3	639	8	B2922748	B2922748 CH240_115
C	42	50.2	5.2	466	8	B17827	B17827 347119_TPB
C	43	48.8	5.1	852	7	CN835976	CN835976 AGENCOURT
C	44	47.4	5.0	776	8	B2842365	B2842365 CH240_239
C	45	45.8	4.8	921	7	CN835918	CN835918 AGENCOURT

#### ALIGNMENTS

RESULT 1  
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LOCUS  
DEFINITION  
AGENCOURT 14740222 NIH MGC 145 Homo sapiens cDNA clone  
IMAGE:6971939 5', mRNA sequence.  
CF147792.1 GI:33244060  
EST.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
1 (bases 1 to 717)  
NIH-MGC <http://mgs.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Daniela S. Gerhard, Ph.D.  
Office of Cancer Genomics  
National Cancer Institute / NIH  
Bldg. 31 Rm10A07 Bethesda, MD 20892  
Email: [cgabs-rcmail.nih.gov](mailto:cgabs-rcmail.nih.gov)  
Tissue Procurement: GPCR Consortium  
CDNA Library Preparation: GPCR Consortium  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
<http://image.llnl.gov>  
Plate: IRB102 row e column: 10  
High quality sequence stop: 713.  
Location/Qualifiers  
1. 717

#### FEATURES

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/db\_xref="taxon:9606"  
/clone="IMAGE:6971939"  
/issue\_type="mixed"  
/lab\_host="DH10B"  
/clone\_id="NIH MGC 145"  
/note="Vector: pCDNA3.1; Site 1: varies by clone; Site 2:  
varies by clone; ORFs were PCR-amplified and cloned into  
pCDNA3.1 by the GPCR Consortium. Cloning sites vary by  
clone and include the following: 5'-EcoRV-XmnI/XhoI-3',  
5'-EcoRV-XmnI/NotI-3', EcoRV (TA cloned, non-directional).  
For information about which gene each clones represents,  
please visit our anonymous ftp site at  
[ftp://image.llnl.gov/image/rearrayed\\_plates/IRB1\\_presv.dat](ftp://image.llnl.gov/image/rearrayed_plates/IRB1_presv.dat)

## ORIGIN

a Note: this is a NIH\_MGC Library."

Query Match 9.6%; Score 92; DB 7; Length 717;

Best Local Similarity 51.7%; Pred. No. 1,4e-15; Matches 246; Conservative 0; Mismatches 215; Indels 15; Gaps 1;

QY 53 TCATCTGGTGTACCATTTTACTCCTTTTACGCGCTGTGAGCAATAGCAGCAATGGCTTCA 112  
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 DB 89 TCCTCTTCATGATCATATGATGTGCTTGAGTCCTTGCAATATTTGTGCAAGACGCTTA 148  
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 QY 113 TCACTGCTGCTCTGGGCGGTGAGTGGTGTCTAGGAGAAATGTTGCTTGTGATTA 172  
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 DB 149 TTCTTGAGAGTCTGGGCGAGAAATGCTGCAAGTCAAGAGGCTGATGCTGTGACATGA 208  
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 QY 173 TATTGGTACCTTAAGGGGCGCTGCTGCTGTGCTGAGTGTGTAATGGTAAAGCA 232  
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 DB 209 TTCTCATCAGCCTGGGCGATCTGCTGCTGTCTACAGTGGCGATCATCTGTAACAAAT 268  
 |||||  
 QY 233 TTTATGTTTCTTGATCCGATGCGCTTCCCATACAAACCTGTACTGCACTTTCTAGCTT 292  
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 DB 269 TTTGCTCCTATTTTATTTAATTGATTAATGACTTTGCAAC-----TTAACA 313  
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 QY 293 TCCAGTGGAGTCTTCTGATGCTGACCACTTATGCTCTTACTGCTGATGCTCTTCT 352  
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 DB 314 TCACCTGGGAATTTTAAATATCTCTTACATCTGCTGTTAAACAGCTTGTACCGTGTCT 373  
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 QY 353 ATGTGTGAATAATTTGCTACCTTACCCGATCCGCTCTCTCTGCTTAAAGCAGAAATGT 412  
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 DB 374 ACTGATCAAGAGTCTCTCTTCTTCAACCATACATCTTCTGCTGAGGTGAGAAATTT 433  
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 QY 413 CTGGTGGCTACCATGATGCTCTTCACTCTGAGGGCTCTCCAGCTTGACCAACCATTC 472  
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 DB 434 TGAGGTGTTTCCCTGGATATTACTGGGTTCTGATGATTAATCTGTGTAACAATATCC 493  
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 QY 473 TATTTTTCATAGGCAACCAAGATGTATCAAACTTTAAGAACCATCTACA 528  
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 DB 494 CTTCAGCTATTGGGAATTAATCAATTCAGTTACTACCAATGAGCATCTACCA 549  
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RESULT 2 528 bp DNA linear GSS 17-JUL-2001  
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 LOCUS  
 DEFINITION RPCI-24-375K11.TV RPCI-24 Mus musculus genomic clone  
 ACCESSION RPCI-24-375K11, genomic survey sequence.  
 VERSION BH044856  
 KEYWORDS BH044856.1 GI:14828537  
 SOURCE GSS.  
 ORGANISM Mus musculus (house mouse)  
 Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 528)  
 Zhao, S., Nierman, W., Malek, J., Shatsman, S., Akintet, B., Levins, M.,  
 Tsengaye, G., Geer, K., Krol, M., Shvartsbeyn, A., Gebregeorgis, E.,  
 Russell, D., de Jong, P., and Fraser, C.M.  
 Mouse BAC End Sequences from Library RPCI-24  
 Unpublished (1999)  
 Other\_GSSs: RPCI-24-375K11.TU  
 Contact: Shaying Zhao  
 Department of Eukaryotic Genomics  
 The Institute for Genomic Research  
 9712 Medical Center Dr., Rockville, MD 20850, USA  
 Tel: 301 838 0200  
 Fax: 301 838 0208  
 Email: szhao@tigr.org  
 Clones are derived from the mouse BAC library RPCI-24. For BAC  
 library availability, please contact Pieter de Jong  
 (pdejong@mail.cho.org). Clones may be purchased from BACPAC  
 Resources (http://www.choi.org/bacpac/orderingframe.htm). BAC end  
 page: http://www.tigr.org/tdb/bac\_ends/mouse/bac\_end\_intro.html  
 Plate: 375 row: K column: 11  
 Seq primer: T7

FEATURES  
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 Class: BAC ends.  
 Location/Qualifiers  
 1..528

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 /sex="Male"  
 /cell\_type="Spleen/Brain"  
 /clone\_1b="RPCI-24"  
 /note="Vector: pTARBAcl, Site 1: BamHI, Site 2: BamHI,  
 RPCI-24 Mouse BAC Library produced by Pieter de Jong. The  
 library was cloned in the pTARBAcl cloning vector at the  
 BamHI sites using MboI partially digested male C57BL/6J  
 DNA."

## ORIGIN

Query Match 7.4%; Score 70.6; DB 8; Length 528;  
 Best Local Similarity 50.1%; Pred. No. 3e-09;  
 Matches 175; Conservative 0; Mismatches 174; Indels 0; Gaps 0;

QY 577 TATCTCTCCCTTAATAATGATTAATCTTGACAAATGCCACTGCTCTTTTCAATTG 636  
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 DB 68 TATTTTCGCTGATGATGCTGATGATGATGATGATGATGATGATGATGATGATG 127  
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 QY 637 ATGATTTGCTCATCATCTCTGAGAGACACAGAGAGAGAGAGAGAGAGAGAGAGAG 696  
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 DB 128 ATCATCTTGTCTATGTTCTCATCTGATGATGATGATGATGATGATGATGATGATG 187  
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 QY 697 GGAATCCAGAGAGCCAGTGTGACAGGACACATTAAGGCTGTGCTGCTCTCTTTT 756  
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 DB 188 AGGACTCATGATATACAGACACAGGCTCACATTAATGCTGTGAAGCTTGCCTTCTTC 247  
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 QY 757 GCCATGCTCTTATCTCATATTTCTGTGATGATGATGATGATGATGATGATGATG 816  
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 DB 248 CTCATCTTTATACATCAATACCTGCTCTTACGATATCTGTGACATGCAATTAAT 307  
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 QY 817 CCTGTGACCTTTAAATCTGGGTGGAGAGTCAAGTATTAATCTGTGACAGAGTTTAC 876  
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 DB 308 GTTCACGGTTCCTGACATGCGGCTGGAGAGGTAACTTACATGAGCATCTCATGCA 367  
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 QY 877 CCCATCATCTGCTCTTACAGCACTGACAGGCTGAGAGCTGTGCTGAAGA 925  
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 DB 368 TCCACCATCTGTATTAAGCAACCAAGATGAGAAAGCCCTCAAGA 416  
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RESULT 3 787 bp DNA linear GSS 25-JAN-2001  
 AZ739176/c  
 LOCUS  
 DEFINITION RPCI-24-154D22.TV RPCI-24 Mus musculus genomic clone  
 ACCESSION RPCI-24-154D22, genomic survey sequence.  
 VERSION AZ739176.1 GI:12509031  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 787)  
 Zhao, S., Nierman, W., Malek, J., Shatsman, S., Akintet, B., Levins, M.,  
 Tsengaye, G., Geer, K., Krol, M., Shvartsbeyn, A., Gebregeorgis, E.,  
 Russell, D., de Jong, P., and Fraser, C.M.  
 Mouse BAC End Sequences from Library RPCI-24  
 Unpublished (1999)  
 Other\_GSSs: RPCI-24-154D22.TU  
 Contact: Shaying Zhao  
 Department of Eukaryotic Genomics  
 The Institute for Genomic Research  
 9712 Medical Center Dr., Rockville, MD 20850, USA  
 Tel: 301 838 0200  
 Fax: 301 838 0208  
 Email: szhao@tigr.org



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: February 4, 2005, 14:27:28 ; Search time 4374 Seconds  
(without alignments)  
10601.656 Million cell updates/sec

Title: US-10-628-464-1

Perfect score: 957

Sequence: 1 atgaatggagacacatggt.....caagtggtggacacttga 957

Scoring table: OLIGO\_NUC

Gapop 60.0 , Gapext 60.0

Searched: 4708233 seqs, 24227607955 residues

Word size : 0

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

GenEmbl:\*  
1: gb\_ba:\*  
2: gb\_hgt:\*  
3: gb\_in:\*  
4: gb\_cm:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_dr:\*  
10: gb\_ro:\*  
11: gb\_sts:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vi:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	957	100.0	957	AY724955	AY724955 Homo sapi
2	929	97.1	954	BD171274	BD171274 Novel G p
3	929	97.1	954	BD185566	BD185566 Novel G p
4	929	97.1	957	CQ738424	CQ738424 Sequence
5	929	97.1	957	CQ800046	CQ800046 Sequence
6	929	97.1	957	AY114094	AY114094 Homo sapi
7	929	97.1	72045	AC092214	AC092214 Homo sapi
8	437	45.7	957	AY724901	AY724901 Pan trogl
9	419	43.8	957	AY724866	AY724866 Pan panis
10	176	18.4	957	AY724923	AY724923 Gorilla g
11	114	11.9	957	AY724986	AY724986 Pongo pyg
12	81	8.5	957	AY725022	AY725022 Macaca mu
13	47	4.9	131565	AC143122	AC143122 Macaca mu
14	26	2.7	26	BD171279	BD171279 Novel G p
15	26	2.7	26	BD185571	BD185571 Novel G p
16	26	2.7	32	BD171275	BD171275 Novel G p
17	26	2.7	32	BD185567	BD185567 Novel G p
18	25	2.6	32	BD171276	BD171276 Novel G p
19	25	2.6	32	BD185568	BD185568 Novel G p

20	23	2.4	6	BD171277	BD171277 Novel G p
21	23	2.4	6	BD185569	BD185569 Novel G p
22	23	2.4	224803	AC111351	AC111351 Rattus no
23	23	2.4	252616	AC122593	AC122593 Rattus no
24	22	2.3	22	BD171278	BD171278 Novel G p
25	22	2.3	22	BD185570	BD185570 Novel G p
26	22	2.3	966	AF532748	AF532748 Rattus no
27	22	2.3	966	AF532786	AF532786 Mus muscu
28	22	2.3	111375	AC1073878	AC1073878 Homo sapi
29	22	2.3	203639	AC117625	AC117625 Mus muscu
30	22	2.3	216647	CNS057CO	AL355773 Human chr
31	22	2.3	218921	AC097912	AC097912 Rattus no
32	22	2.2	433	CQ452267	CQ452267 Sequence
33	21	2.2	618	CQ746689	CQ746689 Sequence
34	21	2.2	119563	HS1894012	AL078608 Human DNA
35	21	2.2	123039	AC093087	AC093087 Homo sapi
36	21	2.2	148687	AC021636	AC021636 Homo sapi
37	21	2.2	184918	AC114608	AC114608 Mus muscu
38	21	2.2	191540	AC144780	AC144780 Pan trogl
39	21	2.2	191924	AC091440	AC091440 Homo sapi
40	21	2.2	197439	AC133441	AC133441 Rattus no
41	21	2.2	212858	AC124475	AC124475 Mus muscu
42	21	2.2	214439	AC137211	AC137211 Rattus no
43	21	2.2	230926	AC114457	AC114457 Rattus no
44	21	2.2	232848	AC136675	AC136675 Rattus no
45	21	2.2	234826	AC093340	AC093340 Mus muscu

# ALIGNMENTS

RESULT 1  
AY724955 957 bp DNA linear PRI 18-SEP-2004  
LOCUS Homo sapiens chromosome 7 taste receptor T2R56 gene, complete cds.  
DEFINITION AY724955  
ACCESSION AY724955.1 GI:51989208  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE  
AUTHORS Anne, F., Yoav, G., Orna, M. and Svante, P.  
TITLE Evolution of bitter taste receptors in human and apes  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 957)  
AUTHORS Anne, F., Yoav, G., Orna, M. and Svante, P.  
TITLE Direct Submission  
JOURNAL Submitted (12-AUG-2004) Genetics, Max-Planck Institute for Evolutionary Anthropology, Deutscher Platz 6, Leipzig 04103, Germany

FEATURES  
source Location/Qualifiers  
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IGNHRVONYLNLQPMVATGDSIRSYCEKFLPLKMTITMTPAVAFICMLIT  
SIGRRHKALITTSGRSPVOAHIKALIALSPMLPFSYSLVFSAAAGFPPDPF  
KRWVESVYILCAVAHPITLLFSNCRIRAVLKSRRSRRCGTP"

# ORIGIN

Query Match 100.0%; Score 957; DB 9; Length 957;  
Best Local Similarity 100.0%; Pred. No. 0;

Matches 957; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGATGAGACACCATGGTTCTAGAGTCTTGGTGACTGACAGAAGGCCATCATCTTG 60  
DB 1 ATGATGAGACACCATGGTTCTAGAGTCTTGGTGACTGACAGAAGGCCATCATCTTG 60

QY 61 GTTACCATTTTACTCCTTTTACGCTGTGTAGCAATAGCAGGCAATGGCTTCATCTGCT 120  
DB 61 GTTACCATTTTACTCCTTTTACGCTGTGTAGCAATAGCAGGCAATGGCTTCATCTGCT 120

QY 121 GCTCTGGGCGGTGAGGAGTGTGCTACGAGAAATGTGTGGCTTGTGATTAATGTTGTT 180  
DB 121 GCTCTGGGCGGTGAGGAGTGTGCTACGAGAAATGTGTGGCTTGTGATTAATGTTGTT 180

QY 181 AGCTTAGGGGCTCTGCTCTGTGTGACAGTGTGTAATGGGTAAGACATTTATGTT 240  
DB 181 AGCTTAGGGGCTCTGCTCTGTGTGACAGTGTGTAATGGGTAAGACATTTATGTT 240

QY 241 TTCTTGATCCGATGGGCTTCCATACACCTGTGACAGTTTCTAGCTTTCCAGTGG 300  
DB 241 TTCTTGATCCGATGGGCTTCCATACACCTGTGACAGTTTCTAGCTTTCCAGTGG 300

QY 301 GACTTCTGAAATGCTGACACCTTATGATCTCTACCTGCTCAGTGTCTTCTATGTTG 360  
DB 301 GACTTCTGAAATGCTGACACCTTATGATCTCTACCTGCTCAGTGTCTTCTATGTTG 360

QY 361 AAAATTGCTACTTCAACCCGCTGTCTTCTGCTTAAGACACAAGTTGCTGGGTGG 420  
DB 361 AAAATTGCTACTTCAACCCGCTGTCTTCTGCTTAAGACACAAGTTGCTGGGTGG 420

QY 421 CTACATGATGATGCTTCACTCTGTAGAGGCTGTCCAGCTTCAACACATTTCTATTTTC 480  
DB 421 CTACATGATGATGCTTCACTCTGTAGAGGCTGTCCAGCTTCAACACATTTCTATTTTC 480

QY 481 ATAGGCAACCAAGATGTATCAAGAACTATTAAAGAACCATCTACACCTTGAATGTC 540  
DB 481 ATAGGCAACCAAGATGTATCAAGAACTATTAAAGAACCATCTACACCTTGAATGTC 540

QY 541 ACTGCGATAGCATACGAGCTACTGTGAGAAATTTCTATCTTCTCCCTTAATAATGATT 600  
DB 541 ACTGCGATAGCATACGAGCTACTGTGAGAAATTTCTATCTTCTCCCTTAATAATGATT 600

QY 601 ACTTGGACAAATGCCACTGTGTCTTTTTCATTTTTCATTTGATGATTTGCTCATCATCTG 660  
DB 601 ACTTGGACAAATGCCACTGTGTCTTTTTCATTTTTCATTTGATGATTTGCTCATCATCTG 660

QY 661 GGAAGACACAGGAAGAGGCTCTCTTACAACTCAGAGATTCGAGAGCCAGTGTGAG 720  
DB 661 GGAAGACACAGGAAGAGGCTCTCTTACAACTCAGAGATTCGAGAGCCAGTGTGAG 720

QY 721 GCACACATAAAGGCTGTGAGCTCTCTCTTTTGGCAGTGTCTTTCATCTCATATTTTC 780  
DB 721 GCACACATAAAGGCTGTGAGCTCTCTCTTTTGGCAGTGTCTTTCATCTCATATTTTC 780

QY 781 CTGTCACTGTGTGATGCTGTGAGGATTTTTCACCTTGTGACCTTTAAATCTGGGTG 840  
DB 781 CTGTCACTGTGTGATGCTGTGAGGATTTTTCACCTTGTGACCTTTAAATCTGGGTG 840

QY 841 TGGGATCACTGATTTATCTGTGTGAGAGTTCACCCCATCATTTGCTCTTACAGAAC 900  
DB 841 TGGGATCACTGATTTATCTGTGTGAGAGTTCACCCCATCATTTGCTCTTACAGAAC 900

QY 901 TGGAGGCTGAGCTGTGAGAGTGTGCTTCCCTCAAGGTGTGGGACACCTTGA 957  
DB 901 TGGAGGCTGAGCTGTGAGAGTGTGCTTCCCTCAAGGTGTGGGACACCTTGA 957

RESULT 2  
LOCUS BD171274 954 bp DNA linear PAT 17-JAN-2003  
DEFINITION Novel G protein-coupled receptor protein and DNA thereof.  
ACCESSION BD171274  
VERSION BD171274.1 GI:27877086

KEYWORDS WO 02057309-A/1.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE 1 (bases 1 to 954)  
AUTHORS Miwa,M., Ito,T., Shintani,Y. and Miyajima,N.  
TITLE Novel G protein-coupled receptor protein and DNA thereof  
JOURNAL Patent: WO 02057309-A 1 25-JUL-2002;  
TAKEDA CHEMICAL INDUSTRIES LTD,MASANORI MIWA,TAKASHI ITO, YASUSHI SHINTANI, NOBUYUKI MIYAJIMA  
COMMENT OS Homo sapiens (human)  
PN WO 02057309-A/1  
PD 25-JUL-2002  
PE 17-JAN-2002 WO 2002JP000271  
PR 18-JAN-2001 JP 01P 010814.30-MAR-2001 JP 01P 102558 PI  
MASANORI MIWA,TAKASHI ITO,YASUSHI SHINTANI,NOBUYUKI MIYAJIMA PC  
C07K14/705,C12N15/09,C12N1/15,C12N1/21,C12N5/10, PC  
C07K16/28,  
PC C12P21/02,C12P21/08,C12Q1/02,C12Q1/68,G01N33/15,G01N33/53, PC  
G01N33/566,  
PC  
A61K38/00,A61K45/00,A61P1/00,A61P3/00,A61P5/00,A61P9/00,A61P11/ PC  
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PC A61P25/28,A61P35/00,A61P37/00  
CC Novel G protein-coupled receptor protein and DNA thereof FH  
Key Location/Qualifiers  
FT source 1..954  
FT location/Qualifiers  
/organism='Homo sapiens (human)'.  
/organism='Homo sapiens'  
/mol\_type='genomic DNA'  
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ORIGIN  
Query Match 97.1%; Score 929; DB 6; Length 954;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 929; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGATGAGACACCATGGTTCTAGAGTCTTGGTGACTGACAGAAGGCCATCATCTTG 60  
DB 1 ATGATGAGACACCATGGTTCTAGAGTCTTGGTGACTGACAGAAGGCCATCATCTTG 60

QY 61 GTTACCATTTTACTCCTTTTACGCTGTGTAGCAATAGCAGGCAATGGCTTCATCTGCT 120  
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QY 121 GCTCTGGGCGGTGAGGAGTGTGCTACGAGAAATGTGTGGCTTGTGATTAATGTTGTT 180  
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Qy 901 TGGAGGCTGAGAGCTGTGCTGAAGAGTGG 929

Db 901 TGGAGGCTGAGAGCTGTGCTGAAGAGTGG 929

LOCUS	BD185566	954 bp	DNA	linear	PAT 17-JUN-2003
DEFINITION	Novel G protein-coupled receptor and its DNA.				
VERSION	BD185566.1	GI:31877766			
KEYWORDS	JP 2002360279-A/1.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo. 1 (bases 1 to 954)				
AUTHORS	Miwa,M., Ito,T., Shintani,Y. and Miyajima,N.				
TITLE	Novel G protein-coupled receptor and its DNA				
JOURNAL	Patent: JP 2002360279-A 1 17-DEC-2002; TAKEDA CHEMICAL INDUSTRIES LTD				
COMMENT	OS Homo sapiens (human) PN JP 2002360279-A/1 PD 17-DEC-2002 PI 17-JAN-2002 JP 2002008445 PM MASANORI MIWA, TAKASHI ITO, YASUSHI SHINTANI, NOBUYUKI MIYAJIMA PC C12N15/09, A61K39/395, A61K45/00, A61P1/00, A61P3/00, A61P5/00, PC A61P9/00, A61P11/00, A61P25/28, A61P29/00, A61P31/00, A61P35/00, PC A61P37/00, PC C07K14/705, C07K16/28, C12N1/15, C12N1/19, C12N1/21, C12N5/10, PC C12P21/02. PC C12Q1/02, C12Q1/68, G01N33/15, G01N33/50, G01N33/53, G01N33/53, PC G01N33/566, PC C12N15/00, C12N5/00 CC Novel G protein-coupled receptor and its DNA FH Location/Qualifiers FT source 1..954 FT /organism='Homo sapiens (human)'. source 1..954 Location/Qualifiers				
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ORIGIN

Query Match	97.1%	Score 929	DB 6	Length 954
Best Local Similarity	100.0%	Pred. No. 0		
Matches 929	Conservative 0	Mismatches 0	Indels 0	Gaps 0

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Db	1	ATGAATGAGACACACATGATCTTCAAGAACTTCGGTGA	CTGCACAAAGAGGCATCATCTTG	60
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Db	61	GTATACAAATTTACTCTCTTTTACGCGCTGGTAGCAATAGCAGGCAATGGCTTATCATCTGCT		120
OY	121	GCTCTGGGCGCTGAGAGTGGGTGCTACGGAAATGATGTTGCGCTTGATGAATGATTAATGGAT		180
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Db	181	AGCCTAAGGGGCGCTCTCGCTTCTGATCTGATCAAGTCAAGTGGTAATGGGTAAGACCATTTATGTT		240
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Db	241	TTCTTGACATCCGATAGCGCTTCCATACAAACCTGTACTGACAGTTTCTAGCTTTCCAGTGG		300
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Db	361	AAATATGCTACTTCAACCAACCCCTGCTCTTCTTGAGCTAAAGACAATGTTGCTGGGTGG		420
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LOCUS	CQ738424	957 bp	DNA
DEFINITION	Sequence 24358 from Patent WO02068579.		linear PAT 03-FEB-2004

ACCESSION CQ738424  
VERSION CQ738424.1 GI:42339256  
KEYWORDS  
SOURCE  
ORGANISM Homo sapiens (human)  
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
AUTHORS Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.  
TITLE Kites, such as nucleic acid arrays, comprising a majority of  
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of theseof  
Patent: WO 02068579-A 24358 06-SEP-2002;  
JOURNAL  
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ORIGIN  
Query Match 97.1%; Score 929; DB 6; Length 957;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 929; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ATGAATGAGACACATGTTCTAGAGATCTTGGTGAAGTGAAGAGAGCCATCATCTTG 60  
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LOCUS  
SEQUENCE 50 from Patent WO2004029087.  
ACCESSION CQ800046  
VERSION CQ800046.1 GI:46848968  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
AUTHORS Bufe, B., Hofmann, T., Krautwurst, D., Kuhn, C. and Meyerhof, W.  
TITLE Bitter taste receptors  
JOURNAL Patent: WO 2004029087-A 50 08-APR-2004;  
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Best Local Similarity 100.0%; Pred. No. 0;  
Matches 929; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ATGAATGAGACACATGTTCTAGAGATCTTGGTGAAGTGAAGAGAGCCATCATCTTG 60  
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DEFINITION Homo sapiens putative taste receptor T2R60 gene, complete cds.  
ACCESSION AY114094  
VERSION AY114094.1 GI:28603637  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM  
REFERENCE  
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
TITLE 1 (bases 1 to 957)  
JOURNAL Conte, C., Ebeling, M., Marcuz, A., Nef, P. and Andres-Barquin, P.J.  
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MEDLINE 22471936  
PUBMED 12584440  
REFERENCE 2 (bases 1 to 957)  
AUTHORS Conte, C., Ebeling, M., Marcuz, A., Nef, P. and Andres-Barquin, P.J.  
TITLE Direct Submission  
JOURNAL Submitted (17-May-2002) Pharma Research Basel, F. Hoffmann-Lia Roche Ltd., Grenzacherstrasse 124, Basel CH-4070, Switzerland  
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## ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0;  
Matches 929; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 7  
AC092214  
LOCUS  
DEFINITION Homo sapiens BAC clone RP11-81109 from 7, complete sequence.  
AC092214  
VERSION AC092214.3  
KEYWORDS HTG.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
AUTHORS  
1 (bases 1 to 72045)  
Hillier, L.W., Fulton, R.S., Fullon, L.A., Graves, T.A., Pepin, K.H., Wagner-McPherson, C., Layman, D., Maas, J., Jaeger, S., Walker, J., Wyllie, K., Sekhon, M., Becker, M.C., O'Laughlin, M.D., Schaller, M.E., Fewell, G.A., Delahunty, K.D., Miner, T.L., Nash, W.E., Cordes, M., Du, H., Sun, H., Edwards, J., Bradshaw-Cordum, H., All, J., Andrews, S., Isak, A., Vanbrunt, A., Nguyen, C., Du, F., Lamar, B., Courtney, L., Kalicki, J., Ozersky, P., Bielicki, L., Scott, K., Holmes, A., Harting, R., Harris, A., Strong, C.M., Hou, S., Tomlinson, C., Dauphin-Kohlberg, S., Kozlowski-Reilly, A., Leonard, S., Kohlfing, T., Rock, S.M., Tin-Mollam, A.M., Abbott, A., Minx, P., Maupin, R., Stromwater, C., Latreille, P., Miller, N., Johnson, D., Murray, J., Moesener, J.P., Wendt, M.C., Yang, S.P., Schultz, B.R., Wallis, J.W., Spiech, T.S., Baertsch, R.A., Brent, M.R., Keibler, E., Fliesch, P., Bork, P., Suyama, M., Bailey, J.A., Portnoy, M.E., Torrents, D., Chinaiella, A.T., Gish, W.R., Eddy, S.R., McPherson, J.D., Olson, M.V., Eichler, E., Green, E.D., Waterston, R.H. and Wilson, R.K.  
The DNA sequence of human chromosome 7  
Nature 424 (6945), 157-164 (2003)

TITLE  
JOURNAL  
MEDLINE  
22737999  
12853948

REFERENCE  
AUTHORS  
2 (bases 1 to 72045)  
Doebber, A., Elliott, G., Kozlowski, A. and Sun, H.  
The sequence of Homo sapiens BAC clone RP11-81109  
Unpublished (2001)

JOURNAL  
AUTHORS  
3 (bases 1 to 72045)  
Waterston, R.H.  
Direct Submission  
Submitted (29-JUN-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA

REFERENCE  
AUTHORS  
4 (bases 1 to 72045)  
Waterston, R.H.  
Direct Submission  
Submitted (15-NOV-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA

JOURNAL  
AUTHORS  
5 (bases 1 to 72045)  
Waterston, R.H.  
Direct Submission  
Submitted (03-JAN-2002) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA

REFERENCE  
AUTHORS  
6 (bases 1 to 72045)  
Waterston, R.H.  
Direct Submission  
Submitted (10-JAN-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA

JOURNAL  
AUTHORS  
7 (bases 1 to 72045)  
Wilson, R.  
Direct Submission  
Submitted (31-JAN-2004) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA

COMMENT  
On Nov 15, 2001 this sequence version replaced gi:15625026.

----- Genome Center  
Center: Washington University Genome Sequencing Center  
Center code: WUGSC  
Web site: <http://genome.wustl.edu>  
Contact: [sapiens@genome.wustl.edu](mailto:sapiens@genome.wustl.edu)  
----- Summary Statistics  
Center project name: H\_NH081109  
-----

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:  
all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:  
The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 7 Mapping Project (Eric D. Green, Director), John D. McPherson in the Department of Genetics (Washington University), and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see <http://www.nhgri.nih.gov/DIR/GRB/CHR7>, send [mailto:egreen@nhgri.nih.gov](mailto:mailto:egreen@nhgri.nih.gov), or see <http://genome.wustl.edu>

SOURCE INFORMATION:  
The RPC1-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Caranese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. *Genomics* 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at <http://www.chori.org>  
VECTOR: pBAC3.6

NEIGHBORING SEQUENCE INFORMATION:  
The clone sequenced to the left is RP11-563K23 the clone sequenced to the right is RP11-298A10, 2000 bp overlap. Actual start of this clone is at base position 1 of RP11-81109 actual end is at base position 140619 of RP11-298A10.

#### FEATURES

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778. 837  
repeat\_region

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Qy	121	GCTCTGGCGGTGAGACTGGCTGCTACGAGAAATGTTGTTGCTTGTGATTAAGTTATGCT	180				

Db		62937	GCTCTGGGCGTGGAGTGGGGTGCTACGAGAAATGTTGTCCTTGATGAATTAATTGGTT	62996
Oy		181	AGCCTAAGGGCCCTCTGCCTTCTGTCTGCAGTCAGTGTAAATGGGTAAACCATTTATGTT	240
Db		62997	AGCCTAAGGGCCCTCTGCCTTCTGTCTGCAGTCAGTGTAAATGGGTAAACCATTTATGTT	63056
Oy		241	TTCCTTGATGCCAATGAGCCTTCCCATAACAACCCTGATCTAGCACTTTCTACTTTCCAGTGG	300
Db		63057	TTCTTGATCTCCAGATGGCCCTTCCATACCAACCCTGATCTAGCACTTTCTACTTTCCAGTGG	63116
Oy		301	GACTTCCTGAATGCTNCSCAACCTTAATGGTCTCTACCTGAGTCAAGTCTCTTATTTGTGG	360
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Oy		361	AAAATTGCTACCTTCAACCAACCCTGTCTTCTTGCTTAAMACAGAATGTCTGGGTGG	420
Db		63177	AAAATTGCTACCTTCAACCAACCCTGTCTTCTTGCTTAAMACAGAATGTCTGGGTGG	63236
Oy		421	CTAACCATGATGCTCTTTCACGCTCTGTAGGGCTCTCCAGCTTACCAACCATTTTATTTTC	480
Db		63237	CTAACCATGATGCTCTTTCACGCTCTGTAGGGCTCTCCAGCTTACCAACCATTTTATTTTC	63296
Oy		481	ATTAGGCAACCAAGAAATGTATCGAATCTATTAAAGAAACATCTCAACCTTGGAAATGTC	540
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Oy		541	ACTGGCGATAGCAATACGAGAGCTAAGTGTGAAGAAATCTATCTCTCCCTTAATAAATGATT	600
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Oy		661	GGAAGACACAGAAAGAAAGGCTCTCCCTTAACAACCTAGATTTCCGAGGCCAGTGGCAG	720
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Oy		721	GCACACATAAAGGCTCTGCTGCTCCTCTCTCTTTTGCAGATCCTCTTCACTCATATTTTC	780
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Db		63657	TGGAGATCAAGTATTTTATCTGTGTGAGAGATTCACCCCATATCTGTCTTCCAGCAAC	63716
Oy		901	TGCAGGCTGAGAGCTGTGCTGAAGAGTGC	929
Db		63717	TGCAGGCTGAGAGCTGTGCTGAAGAGTGC	63745
RESULT 8				
AY724901				
LOCUS	AY724901	957 bp	DNA	linear PRI 18-SEP-2004
DEFINITION	Pan troglodytes chromosome 7 taste receptor T2R56 gene, complete cds.			
ACCESSION	AY724901			
VERSION	AY724901.1	GI:51989117		
KEYWORDS				
SOURCE	Pan troglodytes (chimpanzee)			
ORGANISM	Pan troglodytes			
REFERENCE	Bukacinski; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Pan. 1 (bases 1 to 957)			
AUTHORS	Anne,F., Yoav,G., Orna,M. and Svante,P.			
TITLE	Evolution of bitter taste receptors in human and apes			
JOURNAL	Unpublished			
REFERENCE	2 (bases 1 to 957)			



AUTHORS Anne, F., Yoav, G., Orna, M. and Svante, P.  
TITLE Direct Submission  
JOURNAL Submitted (12-AUG-2004) Genetics, Max-Planck Institute for  
Evolutionary Anthropology, Deutscher Platz 6, Leipzig 04103,  
Germany

## FEATURES

source

Location/Qualifiers

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/mol\_type="genomic DNA"  
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CDS

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## ORIGIN

Query Match 45.7%; Score 437; DB 9; Length 957;  
Best Local Similarity 99.0%; Pred. No. 4.1e-235;  
Matches 887; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

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34 GTGACGCAAGAAAGGCGCATCTGGTAAACATTTTACTCTTTTAAAGCCGTAAGCA 93  
94 ATAGCAGGCAATGGCTTCATCTGCTGCTG3GCGTGGAGTGGGTCTACGAGAAATG 153  
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94 ATAGCAGGCAATGGCTTCATCTGCTGCTG3GCGTGGAGTGGGTCTACGAGAAATG 153  
154 TTGTTGCTTGTATTAAGTTATTTAGGCTTAAGGGGCTCTGCGTTCTGTCTGACGTCA 213  
154 TTGTTGCTTGTATTAAGTTATTTAGGCTTAAGGGGCTCTGCGTTCTGTCTGACGTCA 213  
214 GTGGTAATGGTAAGCAATTTATTTTCTTGCATCCGATGGCCCTTCCATCAACCCCT 273  
214 GTGGTAATGGTAAGCAATTTATTTTCTTGTATTCGATGGCCCTTCCATCAACCCCT 273  
274 GTACTGAGTTTCTAGCTTCCAGTGGGACTTCCTGAACTCTGCCACCTTATGTTCTCT 333  
274 GTACTGAGTTTCTAGCTTCCAGTGGGACTTCCTGAACTCTGCCACCTTATGTTCTCT 333  
334 ACCTGGCTCAGTGTCTTCTATTTGTGTAATAATTGCTACCTTCAACCCCTGTTCTTCTC 393  
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394 TGCGTAAAGCAAGTTGTGCGGTGCTACATGATGCTCTTCAAGCTCTGTAGAGGCTC 453  
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Db

694 TCAGAGTTCCGAGAGCCAGTGTGACAGGCAACATAAAGGCTGTGAGCTCTCTCTCTCT 753

Qy

754 TTTGGCAGCTCTTATCTCATATTTTCCGTGACAGTGTGACAGTGTGACAGTATTTT 813

Db

754 TTTGGCAGCTCTTATCTCATATTTTCCGTGACAGTGTGACAGTGTGACAGTATTTT 813

Qy

814 CCACCTCTGAGCTTTAAATTTCTGGTGGGAGTCAAGTATTTATCTGTGACAGCT 873

Db

814 CCACCTCTGAGCTTTAAATTTCTGGTGGGAGTCAAGTATTTATCTGTGACAGCT 873

Qy

874 CACCCCATATTCTGCTCTTACAGCAATGACAGCTGAGAGCTGTGCTGAAGCTG 929

Db

874 CACCCCATATTCTGCTCTTACAGCAATGACAGCTGAGAGCTGTGCTGAAGCTG 929

## RESULT 9

LOCUS

AY724866 957 bp DNA linear PRI 18-SEP-2004

DEFINITION

Pan paniscus chromosome 7 taste receptor T2R56 gene, complete cds.

ACCESSION

AY724866

VERSION

AY724866.1 GI:51989057

KEYWORDS

Pan paniscus (pygmy chimpanzee)

SOURCE

Pan paniscus (pygmy chimpanzee)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.

REFERENCE

1 (bases 1 to 957)  
Anne, F., Yoav, G., Orna, M. and Svante, P.  
Evolution of bitter taste receptors in human and apes

JOURNAL

Unpublished  
2 (bases 1 to 957)

AUTHORS

Anne, F., Yoav, G., Orna, M. and Svante, P.

TITLE

Direct Submission  
Submitted (12-AUG-2004) Genetics, Max-Planck Institute for  
Evolutionary Anthropology, Deutscher Platz 6, Leipzig 04103,  
Germany

JOURNAL

Submitted (12-AUG-2004) Genetics, Max-Planck Institute for  
Evolutionary Anthropology, Deutscher Platz 6, Leipzig 04103,  
Germany

FEATURES

Location/Qualifiers

source

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CDS

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## ORIGIN

Query Match 43.8%; Score 419; DB 9; Length 957;  
Best Local Similarity 98.9%; Pred. No. 6.4e-225;  
Matches 919; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

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121 GCTCTGGGCGTGAAGTGGTGTCTACGAGAAATGTTGTTGCTTGTGATTAAGTTAGTT 180  
181 AGCCTAAGGGGCTCTGCTTCTGTCTGACGTGAGTGAATGGTAAGCAATTATGTT 240

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 4, 2005, 13:25:01 ; Search time 622 Seconds  
(without alignments)  
9108.026 Million cell updates/sec

Title: US-10-628-464-1

Perfect score: 957  
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Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 4390206 seqs, 2959870667 residues

Word size : 0

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

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12: geneseqn2004as:.\*  
13: geneseqn2004bs:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	929	97.1	954	6	ABK87584 DNA encod
2	929	97.1	957	12	ADJ87104 Nucleotid
3	929	97.1	957	13	ADM33336 Human bit
4	26	2.7	26	6	ABK87589 Novel hum
5	26	2.7	32	6	ABK87585 Novel hum
6	25	2.6	32	6	ABK87586 Novel hum
7	23	2.4	23	6	ABK87587 Novel hum
8	22	2.3	22	6	ABK87588 Novel hum
9	22	2.3	939	8	ACC44449 Gene enco
10	21	2.2	433	6	ABN24775 Human ORF
11	21	2.2	954	10	ADB07626 Novel cod
12	20	2.1	686	6	ABQ65740 Arabidops
13	20	2.1	879	3	AAC40611 Arabidops
14	20	2.1	1235	3	AAZ52509 Human sec
15	20	2.1	13308	6	AAK98531 Human eno
16	19	2.0	248	4	AAI56241 Probe #24
17	19	2.0	248	4	AAK24246 Human bra
18	19	2.0	248	4	ABS49918 Human liv
19	19	2.0	248	6	ABS23758 Human gen
20	19	2.0	263	4	AAI22458 Probe #12

C 21	19	2.0	263	4	ABA67533 Human foe
C 22	19	2.0	263	4	AAI47750 Probe #16
C 23	19	2.0	263	4	ABA49632 Human bre
C 24	19	2.0	263	4	ABA34615 Probe #13
C 25	19	2.0	263	4	AAK41705 Human bon
C 26	19	2.0	263	4	AAK15959 Human bra
C 27	19	2.0	263	4	AB841294 Human liv
C 28	19	2.0	263	5	AAI08145 Probe #81
C 29	19	2.0	263	6	ABS15711 Human gen
C 30	19	2.0	387	4	AAI13223 Probe #31
C 31	19	2.0	387	4	ABA54921 Human foe
C 32	19	2.0	387	4	AAI14576 Probe #32
C 33	19	2.0	387	4	ABA44481 Human bre
C 34	19	2.0	387	4	ABA24690 Probe #31
C 35	19	2.0	387	4	AAK28650 Human bon
C 36	19	2.0	387	4	AAK03196 Human bra
C 37	19	2.0	387	4	ABS28246 Human liv
C 38	19	2.0	387	5	AAI03129 Probe #31
C 39	19	2.0	387	6	ABS03158 Human gen
C 40	19	2.0	485	4	AAI10206 Probe #13
C 41	19	2.0	485	4	ABA51843 Human foe
C 42	19	2.0	485	4	AAI131458 Probe #14
C 43	19	2.0	485	4	ABA21670 Probe #13
C 44	19	2.0	485	4	AAK25586 Human bon
C 45	19	2.0	485	4	AAK00146 Human bra

## ALIGNMENTS

RESULT 1	ABK87584	standard; cDNA; 954 BP.
ID	ABK87584	standard; cDNA; 954 BP.
AC	ABK87584;	
XX	24-SEP-2002	(first entry)
DE	DNA encoding novel human G-protein coupled receptor.	
XX	G-protein coupled; receptor; liver; central nervous system disease;	
KW	Alzheimer's disease; anorexia; dementia; metabolic disease; diabetes;	
KW	hyperlipemia; cancer; non-small cell lung cancer; ovarian cancer;	
KW	stomach cancer; breast cancer; colon cancer; bladder cancer; rheumatism;	
KW	circulatory disease; hypertension; atherosclerosis; angina; allergy;	
KW	inflammatory disease; respiratory disease; asthma; bronchitis;	
KW	digestive disease; stomach ulcer; duodenal ulcer; immune disorder;	
KW	autoimmune disease; infection; acquired immunodeficiency syndrome; AIDS;	
KW	pneumonia; influenza; gene; ss.	
OS	Homo sapiens.	
XX		
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FT		/partial
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XX	17-JAN-2002; 2002WO-JP000271.	
XX	18-JAN-2001; 2001JP-00010814.	
PR	30-MAR-2001; 2001JP-00102558.	
XX	(TAKE ) TAKEDA CHEM IND LTD.	
PA		
XX		
XX	Miwa M, Ito T, Shintani Y, Miyajima N;	
PI		
XX	WPI; 2002-538457/57.	

DR P-PSDB; AAU98514.  
 XX New G-protein coupled receptor protein expressed in human liver for  
 PT design of drugs and reagents for treatment and diagnosis of cancer and  
 PT respiratory metabolic and other diseases.  
 XX  
 PS Claim 6; Page 91; 101pp; Japanese.  
 XX  
 CC The invention describes a novel G-protein coupled receptor protein  
 CC expressed in human liver. The protein is used in the treatment.  
 CC prevention and diagnosis of central nervous system diseases (such as  
 CC Alzheimer's, anorexia and dementia), metabolic diseases (such as diabetes  
 CC and hyperlipaemia), cancer (such as non-small cell lung cancer, ovarian  
 CC cancer, stomach cancer, breast cancer, colon cancer and bladder cancer),  
 CC circulatory diseases (such as hypertension, atherosclerosis and angina),  
 CC inflammatory diseases (such as allergy and rheumatism), respiratory  
 CC diseases (such as asthma and bronchitis), digestive diseases (such as  
 CC stomach ulcer and duodenal ulcer), immune disorders (such as autoimmune  
 CC diseases), and infections (such as acquired immunodeficiency syndrome  
 CC (AIDS), pneumonia and influenza). This sequence encodes the novel G-  
 CC protein coupled receptor protein described in the invention  
 XX  
 XX  
 SQ Sequence 954 BP; 202 A; 241 C; 214 G; 297 T; 0 U; 0 Other;  
 Query Match 97.1%; Score 929; DB 6; Length 954;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 929; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 ATGAATGGAGACACAGATGGTTCTAGATCTTCGGTACTACAGAAAGGCCATCATCTTG 60  
 DB 1 ATGAATGGAGACACAGATGGTTCTAGATCTTCGGTACTACAGAAAGGCCATCATCTTG 60  
 QY 61 GTTACCATTTTACTCTTTTACGCTGTAGCAATAGCAGCAATGGCTTCATCACTGCT 120  
 DB 61 GTTACCATTTTACTCTTTTACGCTGTAGCAATAGCAGCAATGGCTTCATCACTGCT 120  
 QY 121 GCTCTGGGCGCTGGAGTGGTGCTACGAGAAATGTTGCTCTGTGTAATGATTGCTT 180  
 DB 121 GCTCTGGGCGCTGGAGTGGTGCTACGAGAAATGTTGCTCTGTGTAATGATTGCTT 180  
 QY 181 AGCCTAGGGGCGCTGCTCTGTCTGTCGACATGAGTGTATGGGTAAAGACATTATGTT 240  
 DB 181 AGCCTAGGGGCGCTGCTCTGTCTGTCGACATGAGTGTATGGGTAAAGACATTATGTT 240  
 QY 241 TTCTTGATCCGATGGCTTCCCATACACCTGTAAGTGAAGTTTCAAGTTTCCAGTGG 300  
 DB 241 TTCTTGATCCGATGGCTTCCCATACACCTGTAAGTGAAGTTTCAAGTTTCCAGTGG 300  
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 DB 301 GACTTCTGTAATGCTGCGACCTTATGCTCTTACTGCTGCTCAAGTGTCTTATTTGTTG 360  
 QY 361 AAAATTGCTACTTTCACCCACCGTCTTCTGCTGTAAGACAAATGTTCTGGGTGG 420  
 DB 361 AAAATTGCTACTTTCACCCACCGTCTTCTGCTGTAAGACAAATGTTCTGGGTGG 420  
 QY 421 CTACCATGATGCTCTTCACTCTGTAGGGCTCTCCAGCTTCCACCATTTATTTTTC 480  
 DB 421 CTACCATGATGCTCTTCACTCTGTAGGGCTCTCCAGCTTCCACCATTTATTTTTC 480  
 QY 481 ATAGGCAACCAAGATGTATCAAGAACTATTTAAGAACCATTTACAACTTGGAAATGTC 540  
 DB 481 ATAGGCAACCAAGATGTATCAAGAACTATTTAAGAACCATTTACAACTTGGAAATGTC 540  
 QY 541 ACTGGGATAGCATAGGAGCTACTGTGAGAAATTTCTTCCCTCTTAAATAAGATTT 600  
 DB 541 ACTGGGATAGCATAGGAGCTACTGTGAGAAATTTCTTCCCTCTTAAATAAGATTT 600  
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 QY 661 GGAAGACACAGAAAGAGGCTTCTCTTAAACCTCAGGATTCGAGAGCCCAAGTGTGAC 720

DB 661 GGAAGACACAGAAAGAGGCTTCTCTTAAACCTCAGGATTCGAGAGCCCAAGTGTGAC 720  
 QY 721 GCACATATAAGAGCTGTGCTGAGCTCTCTCTCTTTTGGCAGTCTCTTATCATATTTTC 780  
 DB 721 GCACATATAAGAGCTGTGCTGAGCTCTCTCTCTTTTGGCAGTCTCTTATCATATTTTC 780  
 QY 781 CTGTCACTGGTGTTCAGTCTGACGTAGATTTTTCACCTCTGACCTTAAATTTGGGTG 840  
 DB 781 CTGTCACTGGTGTTCAGTCTGACGTAGATTTTTCACCTCTGACCTTAAATTTGGGTG 840  
 QY 841 TGGGAGTCACTGATTTATCTGTGTGACAGATTACCCCATCATTTTGTCTTTCAGCAAC 900  
 DB 841 TGGGAGTCACTGATTTATCTGTGTGACAGATTACCCCATCATTTTGTCTTTCAGCAAC 900  
 QY 901 TGCAGGCTGAGAGCTGTGCTGGAAGTGC 929  
 DB 901 TGCAGGCTGAGAGCTGTGCTGGAAGTGC 929

## RESULT 2

ADJ87104

ADJ87104 standard; DNA; 957 BP.

ADJ87104;

06-MAY-2004 (first entry)

Nucleotide sequence of human bitter taste receptor T2R76.

Human, bitter taste receptor ; T2R76; chromosome 7; bitter taste ; ss.

Homo sapiens.

Key Location/Qualifiers

FT CDS 1..957

FT /tag= a

FT /product= "bitter taste receptor T2R76"

PD MO2004011617-A2.

PD 05-FEB-2004.

PF 29-JUL-2003; 2003WO-US023604.

PR 29-JUL-2002; 2002US-0398727P.

XX (SENO-) SENOMYX INC.

XX (ADLER/) ADLER J E.

XX (TANG/) TANG H.

XX (PRON/) PRONIN A.

XX (ZOLL/) ZOLLER M.

PI Adler JE, Tang H, Pronin A, Zoller M;

XX MPI; 2004-143845/14.

XX P-PSDB; ADJ87105.

PT Novel isolated bitter taste receptor, T2R76 polypeptide useful for

XX identifying modulators of taste perception, or bitter compounds.

XX Claim 1; Page 97-98; 100pp; English.

XX The present sequence encodes human bitter taste receptor T2R76. The human

XX T2R76 gene is located on chromosome 7 in the region 144062692-144063648.

XX The reading frame of T2R76 is intronless. T2R76 polypeptides and

XX polynucleotides are useful for identifying modulators. Such modulators

XX are useful for modulating bitter taste perception in a subject. T2R76

XX agonists can be administered to enhance bitter tastes, while T2R76

XX antagonists can be administered to reduce bitter taste.

XX Sequence 957 BP; 203 A; 241 C; 215 G; 298 T; 0 U; 0 Other;

Query Match 97.1%; Score 929; DB 12; Length 957;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 929; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 ATGAAATGAGACCAACATGTTCTAGATCTTGGTGAAGTGAACAAGAGGCCATCATCTTG 60
QY 61 GTTACCACTTTTACTCCCTTTTAAAGCTGTGTAGCAATACAGCAATGGCTTCATCATCTGCT 120
DB 61 GTTACCACTTTTACTCCCTTTTAAAGCTGTGTAGCAATACAGCAATGGCTTCATCATCTGCT 120
QY 121 GCTCTGGGCGGTGAGTGGGTGCTACGAGAGATGTTGTCCTGTGTAGTAAAGTTATGGTT 180
DB 121 GCTCTGGGCGGTGAGTGGGTGCTACGAGAGATGTTGTTGCTGTGTAGTAAAGTTATGGTT 180
QY 181 AGCCTAGAGGCGCTCTGCTCTCTGTCTGAGTCACTGTGTAAAGGTAAGACATTTATGTT 240
DB 181 AGCCTAGAGGCGCTCTGCTCTCTGTCTGAGTCACTGTGTAAAGGTAAGACATTTATGTT 240
QY 241 TTCTTGATCCGATGAGGCTTCCCATACACCTGTACTGCAATTTTCACTTTTCACTG 300
DB 241 TTCTTGATCCGATGAGGCTTCCCATACACCTGTACTGCAATTTTCACTTTTCACTG 300
QY 301 GACTTCTGATGCTGCGACCTTATGATGCTCTACCTGAGTCACTGTCTTCTATTTGTTG 360
DB 301 GACTTCTGATGCTGCGACCTTATGATGCTCTACCTGAGTCACTGTCTTCTATTTGTTG 360
QY 361 AAAATTGCTACCTTACCCACCCCTGTCTTCTTCTGCTTAAAGCAAGTTGTCTGGGTG 420
DB 361 AAAATTGCTACCTTACCCACCCCTGTCTTCTTCTGCTTAAAGCAAGTTGTCTGGGTG 420
QY 421 CTACACATGATGCTCTTCACTGTGTAGGAGTCTCCAGCTTCAACACATTTATTTTC 480
DB 421 CTACACATGATGCTCTTCACTGTGTAGGAGTCTCCAGCTTCAACACATTTATTTTC 480
QY 481 ATAGGCAACCAACAGATGTATCAGACATTTTAAAGAACATCTACAACTTGGATGTC 540
DB 481 ATAGGCAACCAACAGATGTATCAGACATTTTAAAGAACATCTACAACTTGGATGTC 540
QY 541 ACTGGCGATGACATACGAGAGTCTGTAGAAATTTATCTTCCCTTAAAAATGAT 600
DB 541 ACTGGCGATGACATACGAGAGTCTGTAGAAATTTATCTTCCCTTAAAAATGAT 600
QY 601 ACTTGGACATGCCCATCTGCTCTTTTTCATTTGCAATGTTTGTCTATCATCTCTG 660
DB 601 ACTTGGACATGCCCATCTGCTCTTTTTCATTTGCAATGTTTGTCTATCATCTCTG 660
QY 661 GGAAGACACAGAAAGAGGCTCTCTTACAACTCAGGATTCGAGAGGCCAGTGTGAG 720
DB 661 GGAAGACACAGAAAGAGGCTCTCTTACAACTCAGGATTCGAGAGGCCAGTGTGAG 720
QY 721 GCACACATTAAGGCTCTGCTGCTCTCTCTCTTTTGGCAAGCTTCATCATCATTTTC 780
DB 721 GCACACATTAAGGCTCTGCTGCTCTCTCTCTTTTGGCAAGCTTCATCATCATTTTC 780
QY 781 CTGTCACTGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840
DB 781 CTGTCACTGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840
QY 841 TGGAGTCAGTGAATTTATCTGTGTGAGCAAGTTACCCCATCATTTCTGCTTTCAGCAAC 900
DB 841 TGGAGTCAGTGAATTTATCTGTGTGAGCAAGTTACCCCATCATTTCTGCTTTCAGCAAC 900
QY 901 TGCAGGCTGAGAGCTGTGCTGTAAGAGTGC 929
DB 901 TGCAGGCTGAGAGCTGTGCTGTAAGAGTGC 929
  
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RESULT 3  
 ADM3336  
 ID ADM3336 standard; cDNA; 957 BP.  
 XX

AC ADM33336;  
 XX  
 DT 18-NOV-2004 (first entry)  
 XX  
 DE Human bitter taste receptor TAS2R60 encoding cDNA SEQ ID NO:50.  
 XX  
 KM human; bitter taste receptor; food; gene; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT 1.957  
 FT CDS /\*tag= a  
 FT /product= "bitter taste receptor hTAS2R60"  
 XX  
 PN NC02004029087-A2.  
 XX  
 PD 08-APR-2004.  
 XX  
 PF 25-SEP-2003; 2003MO-EP010691.  
 XX  
 PR 25-SEP-2002; 2002US-0413298P.  
 XX  
 PA (DBER-) DEUT INST ERNAERUNGSGEFOERCHUNG POTSDAM.  
 PI Bufo B, Hofmann T, Krautwurst D, Kuhn C, Meyerhof W,  
 DR WPI; 2004-305149/28.  
 DR P-PSDB; ADM33335.  
 XX  
 PT Novel bitter receptor polynucleotide encoding human TAS2R protein having  
 PT bitter substance binding activity, useful for producing nutraceutical or  
 PT pharmaceutical compositions comprising antagonists of bitter taste  
 PT receptor activity.  
 XX  
 PS Claim 14; SEQ ID NO 50; 108bp; English.  
 XX  
 CC The present sequence encodes a human bitter taste receptor. Also  
 CC described: (1) a polynucleotide encoding a bitter taste receptor (1); (2)  
 CC a vector (II) containing (1); (3) a host cell (III) genetically  
 CC engineered with (1) or (II); (4) a transgenic non-human animal (IV)  
 CC containing (1), (II) and/or (III); (5) a polypeptide (V) having the amino  
 CC acid sequence encoded by (1) or obtained by culturing (III) and  
 CC recovering polypeptide; (6) an antibody (VII) specifically binding to (V);  
 CC (7) a nucleic acid molecule (VII) specifically hybridizing to (1); (8) an  
 CC antagonist/inhibitor (VIII) against (V) which is antibody, the  
 CC extracellular domain of (V) or its fragment or an inhibiting RNA; (9)  
 CC isolating (M1) an antagonist that binds to (V) encoded by (1); (10)  
 CC isolating (M2) an antagonist of bitter taste receptor activity; (11) a  
 CC foodstuff including human and animal foodstuff, any precursor material or  
 CC additive employed in the production of foodstuff comprising (VII); and  
 CC (12) a nutraceutical/pharmaceutical composition comprising (VII); and an  
 CC active agent and optionally a carrier. (III) is useful for producing a  
 CC polypeptide encoded by (1), which involves culturing (III) and recovering  
 CC the polypeptide encoded by (1). (II) is useful for producing cells  
 CC capable of expressing at least one of the bitter taste receptor  
 CC polypeptide, which involves genetically cells in vitro with (II), where  
 CC the bitter taste receptor polypeptide(s) is/are encoded by (1). (M1) or  
 CC (M2) can be used for producing food or any precursor material or additive  
 CC employed in the production of foodstuffs. (M1) or (M2) can also be used  
 CC for producing nutraceutical or pharmaceutical compositions. (1), (II),  
 CC (VI) or (VIII) can be used for manufacturing a medicament for the  
 CC treatment of an abnormally increased or decreased sensitivity towards a  
 CC bitter substance. The identified agonist/inhibitor efficiently suppresses  
 CC or eliminated bitter tasting components of food and effectively useful in  
 CC food industries.  
 XX  
 SQ Sequence 957 BP; 203 A; 240 C; 215 G; 299 T; 0 U; 0 Other;

Query Match 97.1%; Score 929; DB 13; Length 957;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 929; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ATGAATGAGACCAATGTTCTTCTAGATCTTCGGTACTGACAGAAGGCCATCATCTTG 60
DB 1 ATGAATGAGACCAATGTTCTTCTAGATCTTCGGTACTGACAGAAGGCCATCATCTTG 60
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DB 181 AGCTTAGGGGCTCTCTGCTTCTGTCTGCACTAGTGTGTAAGGTAAGACATTATGTT 240
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DB 301 GACTTCCTGAATGCTGCGACCTTATGATGCTCTACCTGCTCAGTGTCTTCTATGTTG 360
QY 361 AAAATTGCTACCTTCAACCCACCTGTCTTCTGTGGCTAAGACAAGTTGTCTGGGTGG 420
DB 361 AAAATTGCTACCTTCAACCCACCTGTCTTCTGTGGCTAAGACAAGTTGTCTGGGTGG 420
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DB 421 CTACCATGATGCTCTTCACTCTGTAGGGCTCTCCAGCTTCAACCATTTCTATTTTTC 480
QY 481 ATAGGCAACCAAGAAATGTATCAAACTATTTAAGAAACATCTACAACCTTGGAAATGTC 540
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DB 661 GGAAGACACAGAAAGAGGCTCTCTTCAACCTCAGAGATTCGAGAGCCAGTGTGAG 720
QY 721 GCACACATAAAGGCTGTGCTGCTCTCTCTTTTGGCATGCTCTTCAATCTCATATTTC 780
DB 721 GCACACATAAAGGCTGTGCTGCTCTCTCTTTTGGCATGCTCTTCAATCTCATATTTC 780
QY 781 CTGTCACTGTGTCTGATGCTGTGAGGATTTTTCACCTCTGAGACTTTAAATCTGGGTG 840
DB 781 CTGTCACTGTGTCTGATGCTGTGAGGATTTTTCACCTCTGAGACTTTAAATCTGGGTG 840
QY 841 TGGGAGTCACTGATTTATCTGTGTGAGAGATTCAACCCCATCATCTGCTCTCAGAAC 900
DB 841 TGGGAGTCACTGATTTATCTGTGTGAGAGATTCAACCCCATCATCTGCTCTCAGAAC 900
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DB 901 TGCAGGCTGAGAGCTGTGCTGAAGAGTGC 929

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ABK87589 standard; DNA; 26 BP.
XX
AC ABK87589;
XX
DT 24-SEP-2002 (first entry)
XX
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DE Novel human G-protein coupled receptor related probe.
XX
XX G-protein coupled; receptor; liver; central nervous system disease;
XX Alzheimer's disease; anorexia; dementia; metabolic disease; diabetes;
XX hyperlipaemia; cancer; non-small cell lung cancer; ovarian cancer;
XX stomach cancer; breast cancer; colon cancer; bladder cancer; rheumatism;
XX circulatory disease; hypertension; atherosclerosis; angina; allergy;
XX inflammatory disease; respiratory disease; asthma; bronchitis;
XX digestive disease; stomach ulcer; duodenal ulcer; immune disorder;
XX autoimmune disease; infection; acquired immunodeficiency syndrome; AIDS;
XX pneumonia; influenza; probe; ss.
XX
XX Homo sapiens.
XX
XX MO200257309-A1.
XX
XX 25-JUL-2002.
XX
XX 17-JAN-2002; 2002MO-JP000271.
XX
XX 18-JAN-2001; 2001JP-00010814.
XX
XX 30-MAR-2001; 2001JP-00102558.
XX
XX (TAKE ) TAKEDA CHEM IND LTD.
XX
XX Miwa M, Ico T, Shintani Y, Miyajima N;
XX
XX WPI; 2002-538457/57.
XX
XX New G-protein coupled receptor protein expressed in human liver for
XX PT design of drugs and reagents for treatment and diagnosis of cancer and
XX PT respiratory metabolic and other diseases.
XX
XX Example 2; Page 93; 101pp; Japanese.
XX
XX The invention describes a novel G-protein coupled receptor protein
XX CC expressed in human liver. The protein is used in the treatment,
XX CC prevention and diagnosis of central nervous system diseases (such as
XX CC Alzheimer's, anorexia and dementia), metabolic diseases (such as diabetes
XX CC and hyperlipaemia), cancer (such as non-small cell lung cancer, ovarian
XX CC cancer, stomach cancer, breast cancer, colon cancer and bladder cancer),
XX CC circulatory diseases (such as hypertension, atherosclerosis and angina),
XX CC inflammatory diseases (such as allergy and rheumatism), respiratory
XX CC diseases (such as asthma and bronchitis), digestive diseases (such as
XX CC stomach ulcer and duodenal ulcer), immune disorders (such as autoimmune
XX CC disease), and infections (such as acquired immunodeficiency syndrome
XX CC (AIDS), pneumonia and influenza). This sequence represents a probe used
XX CC in the study of the novel G-protein coupled receptor protein described in
XX CC the invention
XX
XX Sequence 26 BP; 7 A; 7 C; 7 G; 5 T; 0 U; 0 Other;
XX
XX Query Match 2.7%; Score 26; DB 6; Length 26;
XX Best Local Similarity 100.0%; Pred.No. 0.036;
XX Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 TGCAGGACACATTAAGGCTGTGCTG 26

RESULT 5
ABK87585 standard; DNA; 32 BP.
XX
AC ABK87585;
XX
DT 24-SEP-2002 (first entry)
XX
XX Novel human G-protein coupled receptor, PCR primer #1.
XX
XX G-protein coupled; receptor; liver; central nervous system disease;
XX KW Alzheimer's disease; anorexia; dementia; metabolic disease; diabetes;
XX
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score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2.1	1235	4	US-09-311-021-69	Sequence 69, Appl
2	2.1	62311	4	US-09-949-016-14582	Sequence 14582, A
3	2.0	4059	4	US-09-774-528-316	Sequence 316, App
4	2.0	42373	4	US-09-949-016-16438	Sequence 16438, A
5	2.0	73519	4	US-09-949-016-16344	Sequence 16344, A
6	2.0	98567	4	US-09-949-016-11750	Sequence 11750, A
7	2.0	105919	4	US-09-949-016-11769	Sequence 11769, A
8	1.9	290	4	US-09-513-999C-153	Sequence 153, App
9	1.9	372	4	US-09-248-796A-4118	Sequence 4118, Ap
10	1.9	381	4	US-09-270-767-14634	Sequence 14634, A
11	1.9	410	4	US-09-513-999C-3046	Sequence 3046, Ap
12	1.9	507	4	US-09-949-016-3571	Sequence 3571, Ap
13	1.9	601	4	US-09-949-016-53362	Sequence 53362, A
14	1.9	601	4	US-09-949-016-93241	Sequence 93241, A
15	1.9	601	4	US-09-949-016-130397	Sequence 130397, A
16	1.9	601	4	US-09-949-016-186250	Sequence 186250, A
17	1.9	601	4	US-09-949-016-186250	Sequence 186250, A
18	1.9	601	4	US-09-949-016-186251	Sequence 186251, A
19	1.9	663	4	US-09-975-327A-3	Sequence 3, Appl
20	1.9	722	3	US-08-998-416-631	Sequence 631, App
21	1.9	820	4	US-09-799-451-742	Sequence 742, App
22	1.9	865	4	US-09-949-016-4339	Sequence 4339, App
23	1.9	892	3	US-08-968-768B-1	Sequence 1, Appl
24	1.9	1891	4	US-09-949-016-1947	Sequence 1947, App
25	1.9	2540	4	US-09-799-451-463	Sequence 463, App
26	1.9	5099	3	US-09-610-040-5	Sequence 5, Appl
27	1.9	5099	4	US-10-267-763-5	Sequence 5, Appl

28	1.9	6759	4	US-09-949-016-13689	Sequence 13689, A
29	1.9	7571	4	US-09-949-016-15313	Sequence 15313, A
30	1.9	52661	4	US-09-949-016-17191	Sequence 17191, A
31	1.9	55226	4	US-09-949-016-14426	Sequence 14426, A
32	1.9	56694	4	US-09-949-016-12568	Sequence 12568, A
33	1.9	56702	4	US-09-949-016-15423	Sequence 15423, A
34	1.9	63644	4	US-09-949-016-12098	Sequence 12098, A
35	1.9	112229	4	US-09-949-016-13144	Sequence 13144, A
36	1.9	136058	4	US-09-949-016-12565	Sequence 12565, A
37	1.9	136480	4	US-09-949-016-17064	Sequence 17064, A
38	1.9	139936	4	US-09-949-016-11782	Sequence 11782, A
39	1.9	139952	4	US-09-949-016-13280	Sequence 13280, A
40	1.9	161652	4	US-09-497-855A-40	Sequence 40, Appl
41	1.9	200663	4	US-09-949-016-12569	Sequence 12569, A
42	1.9	278866	4	US-09-949-016-13922	Sequence 13922, A
43	1.9	278866	4	US-09-949-016-13923	Sequence 13923, A
44	1.9	278866	4	US-09-949-016-13924	Sequence 13924, A
45	1.9	278866	4	US-09-949-016-13925	Sequence 13925, A

#### ALIGNMENTS

```
RESULT 1
US-09-311-021-69
; Sequence 69, Application US/09311021
; Patent No. 6706869
; GENERAL INFORMATION:
; APPLICANT: Wong, Gordon G.
; APPLICANT: Clark, Hilary
; APPLICANT: Fechtel, Kim
; APPLICANT: Agostino, Michael J.
; APPLICANT: Genetics Institute, Inc.
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
; FILE REFERENCE: GI 6300-11A
; CURRENT APPLICATION NUMBER: US/09/311,021
; CURRENT FILING DATE: 1999-05-13
; NUMBER OF SEQ ID NOS: 268
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 69
; LENGTH: 1235
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-311-021-69

Query Match      2.1%; Score 20; DB 4; Length 1235;
Best Local Similarity 100.0%; Pred. No. 6.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 732 |||||
Db 412 GGCTCTGCTGGCTCTCTCT 431

RESULT 2
US-09-949-016-14582/C
; Sequence 14582, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
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SEQ ID NO 14582  
LENGTH: 62311  
TYPE: DNA  
ORGANISM: Human  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)...(62311)  
OTHER INFORMATION: n = A,T,C or G  
US-09-949-016-14582

Query Match 2.0%; Score 20; DB 4; Length 62311;  
Best Local Similarity 100.0%; Pred. No. 7.5;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 132 GGAGTGGGTCTACGAGAA 151  
DB 2244 GGAGTGGGTCTACGAGAA 2225

## RESULT 3

US-09-774-528-316  
Sequence 316, Application US/09774528  
Patent No. 6743619  
GENERAL INFORMATION:  
APPLICANT: Tang, Y. Tom  
APPLICANT: Zhou, Ping  
APPLICANT: Goodrich, Ryle  
APPLICANT: Liu, Chenghua  
APPLICANT: Adundi, Vinod  
APPLICANT: Ren, Feiyan  
APPLICANT: Zhang, Jie  
APPLICANT: Zhao, Qing A.  
APPLICANT: Yang, Yonghong  
APPLICANT: Xue, Aidong J.  
APPLICANT: Wehrman, Tom  
APPLICANT: Wang, Jian-Rui  
APPLICANT: Wang, Jian-Rui  
TITLE OF INVENTION: Dmanac, Radoje T.  
TITLE OF INVENTION: No. 6743619el Nucleic Acids and  
FILE REFERENCE: 802  
CURRENT APPLICATION NUMBER: US/09/774,528  
CURRENT FILING DATE: 2001-01-30  
NUMBER OF SEQ ID NOS: 441  
SOFTWARE: pt\_fl\_genes Version 2.0  
SEQ ID NO 316  
LENGTH: 4059  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (51)...(3131)  
US-09-774-528-316

Query Match 2.0%; Score 19; DB 4; Length 4059;  
Best Local Similarity 100.0%; Pred. No. 22;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 450 GCTCTCAGCTTACACACC 468  
DB 3017 GCTCTCAGCTTACACACC 3035

## RESULT 4

US-09-949-016-16438/C  
Sequence 16438, Application US/09949016  
Patent No. 6812339  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: CL001307  
CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 16438  
LENGTH: 42373  
TYPE: DNA  
ORGANISM: Human  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)...(42373)  
OTHER INFORMATION: n = A,T,C or G  
US-09-949-016-16438

Query Match 2.0%; Score 19; DB 4; Length 42373;  
Best Local Similarity 100.0%; Pred. No. 24;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 655 TCTCTGGGAGACACAGCA 673  
DB 40234 TCTCTGGGAGACACAGCA 40216

## RESULT 5

US-09-949-016-16344  
Sequence 16344, Application US/09949016  
Patent No. 6812339  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: CL001307  
CURRENT APPLICATION NUMBER: US/09/949,016  
CURRENT FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 16344  
LENGTH: 73519  
TYPE: DNA  
ORGANISM: Human  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)...(73519)  
OTHER INFORMATION: n = A,T,C or G  
US-09-949-016-16344

Query Match 2.0%; Score 19; DB 4; Length 73519;  
Best Local Similarity 100.0%; Pred. No. 24;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 582 CTTCCCTTAAATGATT 600  
DB 53035 CTTCCCTTAAATGATT 53053

## RESULT 6

US-09-949-016-11750  
Sequence 11750, Application US/09949016  
Patent No. 6812339  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 4, 2005, 17:40:03 ; Search time 618 Seconds

(without alignments)  
8913.018 Million cell updates/sec

Title: US-10-628-464-1

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Gapop 60.0 , Gapext 60.0

Searched: 4313806 seqs, 287787103 residue

Word size : 0

Total number of hits satisfying chosen parameters: 8627612

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

Published Applications NA:\*

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- 4: /cgn2\_6/prodata/2/pubpna/US06\_PUB\_PUB.seq:\*
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- 19: /cgn2\_6/prodata/2/pubpna/US10\_PUB\_PUB.seq:\*
- 20: /cgn2\_6/prodata/2/pubpna/US11\_PUB\_PUB.seq:\*
- 21: /cgn2\_6/prodata/2/pubpna/US60\_PUB\_PUB.seq:\*
- 22: /cgn2\_6/prodata/2/pubpna/US60\_PUB\_PUB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	957	100.0	957	US-10-628-464-1	Sequence 1, Appl
2	20	2.1	686	US-09-770-149-317	Sequence 317, Ap
3	3	19	248	US-09-864-761-10004	Sequence 30004, A
4	4	19	263	US-09-864-761-19935	Sequence 19935, A
5	5	19	387	US-09-864-761-1156	Sequence 1156, Ap
6	6	19	404	US-10-242-535A-6952	Sequence 6952, Ap
7	7	19	404	US-10-085-783A-6952	Sequence 6952, Ap
8	8	19	479	US-10-027-632-179761	Sequence 179761,
9	9	19	479	US-10-027-632-179762	Sequence 179762,
10	10	19	479	US-10-027-632-179763	Sequence 179763,
11	11	19	479	US-10-027-632-179761	Sequence 179761,

C 12	19	2.0	479	17	US-10-027-632-179762	Sequence 179762,
C 13	19	2.0	479	17	US-10-027-632-179763	Sequence 179763,
C 14	19	2.0	485	9	US-09-864-761-136	Sequence 136, App
C 15	19	2.0	536	9	US-09-864-761-13456	Sequence 13456, A
C 16	19	2.0	883	17	US-10-425-114-3651	Sequence 3651, Ap
C 17	19	2.0	1119	17	US-10-369-493-32521	Sequence 32521, A
C 18	19	2.0	1173	17	US-10-425-114-30814	Sequence 30814, A
C 19	19	2.0	1246	17	US-10-425-114-1158	Sequence 1158, Ap
C 20	19	2.0	1255	18	US-10-425-115-11535	Sequence 11535, Ap
C 21	19	2.0	1866	9	US-09-738-626-2199	Sequence 2199, Ap
C 22	19	2.0	2718	18	US-10-437-963-99200	Sequence 99200, A
C 23	19	2.0	2881	16	US-10-247-671-4	Sequence 4, Appl
C 24	19	2.0	3570	10	US-09-964-295-3	Sequence 3, Appl
C 25	19	2.0	3570	15	US-10-154-419-21	Sequence 21, Appl
C 26	19	2.0	3746	9	US-09-834-973-762	Sequence 762, App
C 27	19	2.0	4059	17	US-10-120-988-316	Sequence 316, App
C 28	19	2.0	4163	17	US-10-291-265-583	Sequence 583, App
C 29	19	2.0	4163	17	US-10-291-265-584	Sequence 584, App
C 30	19	2.0	4205	17	US-10-291-265-111	Sequence 111, App
C 31	19	2.0	4295	17	US-10-291-265-112	Sequence 112, App
C 32	19	2.0	4541	17	US-10-297-633-11	Sequence 11, Appl
C 33	19	2.0	4633	10	US-09-964-295-1	Sequence 1, Appl
C 34	19	2.0	4633	15	US-10-154-419-19	Sequence 19, Appl
C 35	19	2.0	4971	17	US-10-332-447-36	Sequence 36, Appl
C 36	19	2.0	4990	18	US-10-723-860-197	Sequence 197, Appl
C 37	19	2.0	4999	17	US-10-187-975-25	Sequence 25, Appl
C 38	19	2.0	5038	18	US-10-723-860-4939	Sequence 4939, Ap
C 39	19	2.0	5116	17	US-10-187-975-21	Sequence 21, Appl
C 40	19	2.0	5335	17	US-10-187-975-19	Sequence 19, Appl
C 41	19	2.0	5369	17	US-10-187-975-17	Sequence 17, Appl
C 42	19	2.0	5656	17	US-10-187-975-23	Sequence 23, Appl
C 43	19	2.0	5955	18	US-10-490-556-1	Sequence 1, Appl
C 44	19	2.0	31923	18	US-10-490-556-3	Sequence 3, Appl
C 45	19	2.0	3309400	9	US-09-738-626-1	Sequence 1, Appl

#### ALIGNMENTS

RESULT 1  
US-10-628-464-1, Application US/10628464  
; Publication No. US2004012134A1  
; GENERAL INFORMATION:  
; APPLICANT: ADLER, JON ELLIOT  
; APPLICANT: TANG, HUIXIAN  
; APPLICANT: PRONIN, ALEXEY  
; TITLE OF INVENTION: IDENTIFICATION OF A NOVEL BITTER TASTE RECEPTOR, T2R76  
; FILE REFERENCE: 100317.54260US  
; CURRENT APPLICATION NUMBER: US/10/628.464  
; CURRENT FILING DATE: 2003-07-29  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: Patentin Ver. 3.2  
; SEQ ID NO 1  
; LENGTH: 957  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(954)  
US-10-628-464-1

Query Match 100.0%; Score 957; DB 18; Length 957;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 957; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ATGAATGAGACACATGTTCTAGATCTTCGGTACTGACAAAGAGCCATCATCTTG 60  
1 ATGAATGAGACACATGTTCTAGATCTTCGGTACTGACAAAGAGCCATCATCTTG 60  
DB 1 ATGAATGAGACACATGTTCTAGATCTTCGGTACTGACAAAGAGCCATCATCTTG 60  
QY 61 GTTACCATTTTACTCTTTCACCTCTGTAGCATAGCAGGACATGCTTCACTGCT 120  
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DB 61 GTTACCATTTTACTCTTTCACCTCTGTAGCATAGCAGGACATGCTTCACTGCT 120

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QY 121 GCTCTGGGCGTGGAGTGGGTGCTACGAGAGATGTTGTGCTTGTGATTAAGTTATGGTT 180
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Db 121 GCTCTGGGCGGTGGAGTGGGTGCTACGAGAGATGTTGTGCTTGTGATTAAGTTATGGTT 180
QY 181 AGCCTAGGGGCTCTGCTCTTCTGTCTGACAGTCAAGTGTAAATGGGTAAAGCACTTTATGTT 240
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Db 181 AGCCTAGGGGCTCTGCTCTTCTGTCTGACAGTCAAGTGTAAATGGGTAAAGCACTTTATGTT 240
QY 241 TTCTTGATCCGATGGGCTTCCCATACACCCCTGTATCGAGAGTTTCTAGGCTTCCAGTGG 300
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Db 241 TTCTTGATCCGATGGGCTTCCCATACACCCCTGTATCGAGAGTTTCTAGGCTTCCAGTGG 300
QY 301 GACTTCTGAAATGCTGACCTTAAATGCTTAAATGCTTAAATGCTTAAATGCTTAAATGCTT 360
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Db 301 GACTTCTGAAATGCTGACCTTAAATGCTTAAATGCTTAAATGCTTAAATGCTTAAATGCTT 360
QY 361 AAAATTGCTACTTCAACCCACCCCTGCTTCTTCTGCTGCTAAAGCAAGTGTGCTGGGTGG 420
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Db 361 AAAATTGCTACTTCAACCCACCCCTGCTTCTTCTGCTGCTAAAGCAAGTGTGCTGGGTGG 420
QY 421 CTACATGATGATGCTCTTCAAGTCTGTAGGGCTCTCCAGCTTCCACCATTTCTATTTTTC 480
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QY 481 ATAGGCAACCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 540
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QY 541 ACTGGCGATAGCATAGCGAGTACTGTGAGAAATTTCTTCTTCTTCTTCTTCTTCTTCTTCT 600
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Db 541 ACTGGCGATAGCATAGCGAGTACTGTGAGAAATTTCTTCTTCTTCTTCTTCTTCTTCTTCT 600
QY 601 ACTTGACATAGCCCACTGCTGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 660
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Db 661 GGAAGACACAGAGAAAGGCTCTCTTCAACCTCAGAGTTCGAGAGCCAGTGTGCTGAG 720
QY 721 GCACACATTAAGGCTGCTGCTGCTCTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 780
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Db 721 GCACACATTAAGGCTGCTGCTGCTCTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 780
QY 781 CTGTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840
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Db 781 CTGTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840
QY 841 TGGGAGTCAAGTATTTATCTGTGTGAGAGTTCACCCCATTCATCTGCTTCTGAGCAAC 900
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Db 841 TGGGAGTCAAGTATTTATCTGTGTGAGAGTTCACCCCATTCATCTGCTTCTGAGCAAC 900
QY 901 TGCAGGCTGAGAGTGTGCTGAGAGAGTGTCTTCTTCAAGGCTGTGGAGACACTTGA 957
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Db 901 TGCAGGCTGAGAGTGTGCTGAGAGAGTGTCTTCTTCAAGGCTGTGGAGACACTTGA 957

RESULT 2
US-09-770-149-317/c
/ Sequence 317, Application US/09770149
/ GENERAL INFORMATION:
/ APPLICANT: Gorlach, Jörn
/ APPLICANT: An, Yong-Qiang
/ APPLICANT: Hamilton, Carol M.
/ APPLICANT: Price, Jennifer L.
/ APPLICANT: Raines, Tracy M.
/ APPLICANT: Yu, Yang
/ APPLICANT: Rameaka, Joshua G.
/ APPLICANT: Page, Amy
/ APPLICANT: Mathew, Abraham V.
/ APPLICANT: Ledford, Brooke L.
```

```
/ APPLICANT: Moesner, Jeffrey P.
/ APPLICANT: Haas, William David
/ APPLICANT: Garcia, Carlos A.
/ APPLICANT: Kricker, Maja
/ APPLICANT: Slader, Ted
/ APPLICANT: Davis, Keith R.
/ APPLICANT: Allen, Keith
/ APPLICANT: Hoffman, Neil
/ APPLICANT: Hurlan, Patrick
/ APPLICANT: Hurlan, Patrick
/ TITLE OF INVENTION: Expressed Sequences of Arabidopsis
/ TITLE OF INVENTION: thaliana
/ FILE REFERENCE: 2024 (PARA-013PRV)
/ CURRENT APPLICATION NUMBER: US/09/770,149
/ PRIOR FILING DATE: 2001-01-26
/ PRIOR APPLICATION NUMBER: 60/178,506
/ PRIOR FILING DATE: 2000-01-27
/ NUMBER OF SEQ ID NOS: 999
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 317
/ LENGTH: 686
/ TYPE: DNA
/ ORGANISM: Arabidopsis thaliana
US-09-770-149-317

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Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 454 GATGCTCTTCAAGTCTGCTGAG 435

RESULT 3
US-09-864-761-30004/c
/ Sequence 30004, Application US/09864761
/ Patent No. US20020048763A1
/ GENERAL INFORMATION:
/ APPLICANT: Penn, Sharon G.
/ APPLICANT: Rank, David R.
/ APPLICANT: Hanzel, David K.
/ APPLICANT: Chen, Wenheng
/ TITLE OF INVENTION: HUMAN GENOME- DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
/ FILE REFERENCE: Aeomica-X-1
/ CURRENT APPLICATION NUMBER: US/09/864,761
/ CURRENT FILING DATE: 2001-05-23
/ PRIOR APPLICATION NUMBER: US 60/180,312
/ PRIOR FILING DATE: 2000-02-04
/ PRIOR APPLICATION NUMBER: US 60/207,456
/ PRIOR FILING DATE: 2000-05-26
/ PRIOR APPLICATION NUMBER: US 09/632,366
/ PRIOR FILING DATE: 2000-08-03
/ PRIOR APPLICATION NUMBER: GB 24263.6
/ PRIOR FILING DATE: 2000-10-04
/ PRIOR APPLICATION NUMBER: US 60/236,359
/ PRIOR FILING DATE: 2000-09-27
/ PRIOR APPLICATION NUMBER: PCT/US01/00666
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00667
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00664
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00669
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00665
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00668
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00663
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00662
/ PRIOR FILING DATE: 2001-01-30
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Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 389 TCTTCTGCTNAGCAGT 410  
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LOCUS QV0-CT0225-280700-307-e09 CT0225 Homo sapiens cDNA, mRNA sequence.

DEFINITION  
BF334145  
VERSION  
BF334145.1 GI:11304893  
KEYWORDS  
EST.

SOURCE  
Homo sapiens (human)

ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 265)

REFERENCE  
AUTHORS  
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,  
Nagai,M.A., da Silva,M. Jr., Zago,M.A., Bordin,S., Costa,F.F.,  
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,  
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,  
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and  
Simpson,A.J.

TITLE  
Shotgun sequencing of the human transcriptome with ORF expressed  
sequence tags  
JOURNAL  
MEDLINE  
PUBMED  
20202663  
10737800  
Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br  
This sequence was derived from the FAPESP/LICR Human Cancer Genome  
Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV0&t2=QV0-CT0225-  
280700-307-e09&t3=2000-07-28&t4=1)  
Seq primer: puc 18 forward  
High quality sequence start: 19  
High quality sequence stop: 264.

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SmaI; A mini-library was made by cloning products derived  
from ORESTES PCR (U.S. Letters Patent application No.  
196,716 - Ludwig Institute for Cancer Research) profiles  
into the pUC 18 vector. Reverse transcription of tissue  
mRNA and cDNA amplification were performed under low  
stringency conditions."

## ORIGIN

Query Match 2.2%; Score 21; DB 2; Length 265;  
Best Local Similarity 100.0%; Pred. No. 21;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 197 GCTTCTGTCTGCAGTCAGTGG 217  
Db 238 GCTTCTGTCTGCAGTCAGTGG 258

RESULT 3  
CR204857 333 bp DNA linear GSS 06-JUL-2004  
LOCUS CR204857  
DEFINITION Forward strand read from insert in 5'HPRT insertion targeting and  
chromosome engineering clone MHPN144p22, genomic survey sequence.

ACCESSION  
CR204857  
VERSION  
CR204857.1 GI:49983706  
KEYWORDS  
GSS; genome survey sequence; MICE.  
SOURCE  
Mus musculus (house mouse)

ORGANISM  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 333)

REFERENCE  
AUTHORS  
Adams,D.J., Biggs,P.J., Cox,A.V., Davies,R.M., van der Weyden,L.,  
Jonkers,J., Smith,J., Plumb,R.W., Taylor,R.G., Nishijima,I., Yu,Y.,  
Rogers,J. and Bradley,A.

TITLE  
JOURNAL  
Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgehire,  
CB10 1SA, UK. http://www.sanger.ac.uk/MICE  
Location/Qualifiers  
1. 333

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/db\_xref="taxon:10090"  
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/clone\_1b="MHPN"

## ORIGIN

Query Match 2.2%; Score 21; DB 9; Length 333;  
Best Local Similarity 100.0%; Pred. No. 21;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 94 ATGACGAGCATGAGCTTCATC 114  
Db 308 ATGACGAGCATGAGCTTCATC 328

RESULT 4  
BF334124 421 bp mRNA linear EST 22-NOV-2000  
LOCUS QV0-CT0225-191199-058-c08 CT0225 Homo sapiens cDNA, mRNA sequence.  
DEFINITION  
BF334124  
VERSION  
BF334124.1 GI:11304872  
KEYWORDS  
EST.  
SOURCE  
Homo sapiens (human)  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 421)

REFERENCE  
AUTHORS  
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,  
Nagai,M.A., da Silva,M. Jr., Zago,M.A., Bordin,S., Costa,F.F.,  
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,  
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,  
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and  
Simpson,A.J.

TITLE  
Shotgun sequencing of the human transcriptome with ORF expressed  
sequence tags  
JOURNAL  
MEDLINE  
PUBMED  
20202663  
10737800  
Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 4, 2005, 16:58:16 / Search time 168 Seconds  
(without alignments)  
732.082 Million cell updates/sec

Title: US-10-628-464-2  
Perfect score: 1678  
Sequence: 1 MNGDHWLVGSSVTDKKAIL.....SNCRRLRAVLKSRSSRCGTP 318

Scoring table: BIOSIM62  
Gapop 10.0, Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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2	1678	100.0	318	8 ADJ87105	ADJ87105 Amino aci
3	1678	100.0	318	8 ADM33335	ADM33335 Human bit
4	960	57.2	312	6 ABR58013	ABR58013 Mouse GI
5	609	36.3	307	5 AAU11389	AAU11389 Human T2R
6	609	36.3	307	5 ABP95935	ABP95935 Human GPC
7	609	36.3	307	7 ADC86989	ADC86989 Human GPC
8	609	36.3	307	8 ADR29250	ADR29250 Taste rec
9	608	36.2	307	8 ADM33293	ADM33293 Human bit
10	597.5	35.6	308	4 AAB87820	AAB87820 Mouse T2R
11	597.5	35.6	308	4 ADR29216	ADR29216 Taste rec
12	589.5	35.1	308	4 AAB87792	AAB87792 Rat T2R12
13	589.5	35.1	308	4 ADR29160	ADR29160 Taste rec
14	425	25.3	294	6 ABR58017	ABR58017 Rat GI en
15	416	24.8	291	8 ADM33329	ADM33329 Human bit
16	409	24.4	298	6 ABR58014	ABR58014 Mouse GI
17	408	24.3	291	4 AAB87746	AAB87746 Human T2R
18	408	24.3	291	8 ADJ84511	ADJ84511 Human T2R
19	408	24.3	291	8 ADR29091	ADR29091 Taste rec
20	402.5	24.0	293	6 ABR58012	ABR58012 Mouse GI
21	378.5	22.6	318	4 AAB87737	AAB87737 Human T2R
22	378.5	22.6	318	8 ADJ84494	ADJ84494 Human T2R
23	378.5	22.6	318	8 ADQ17322	ADQ17322 Human sof
24	378.5	22.6	318	8 ADQ17199	ADQ17199 Human sof
25	378.5	22.6	318	8 ADR29074	ADR29074 Taste rec

26	378.5	22.6	318	8 ADM33317	ADM33317 Human bit
27	371	22.1	299	4 AAB87812	AAB87812 Mouse T2R
28	371	22.1	299	4 ADR29200	ADR29200 Taste rec
29	359	21.4	312	4 AAB87739	AAB87739 Human T2R
30	359	21.4	312	8 ADJ84498	ADJ84498 Human T2R
31	359	21.4	312	8 ADR29078	ADR29078 Taste rec
32	359	21.4	312	8 ADM33321	ADM33321 Human bit
33	356	21.2	299	4 AAB87783	AAB87783 Rat T2R03
34	356	21.2	299	8 ADJ84452	ADJ84452 Rat T2R G
35	356	21.2	299	8 ADR29142	ADR29142 Taste rec
36	345.5	20.6	312	6 ABR58015	ABR58015 Rat GI en
37	344.5	20.5	297	4 AAB87786	AAB87786 Rat T2R06
38	344.5	20.5	297	8 ADR29148	ADR29148 Taste rec
39	339	20.2	321	5 AAU11382	AAU11382 Human T2R
40	339	20.2	321	7 ADC87279	ADC87279 Human GPC
41	339	20.2	321	8 ADR29236	ADR29236 Taste rec
42	339	20.2	338	5 ABP95933	ABP95933 Human GPC
43	339	20.2	338	7 ADC87333	ADC87333 Human GPC
44	338	20.1	338	5 ABP95934	ABP95934 Human GPC
45	337.5	20.1	309	4 AAB87738	AAB87738 Human T2R

## ALIGNMENTS

RESULT 1  
AAU98514  
ID AAU98514 standard; protein; 318 AA.

AC AAU98514;

DT 24-SEP-2002 (first entry)

DE Novel human G-protein coupled receptor.

XX G-protein coupled; receptor; liver; central nervous system disease;  
XX Alzheimer's disease; anorexia; dementia; metabolic disease; diabetes;  
XX hyperlipaemia; cancer; non-small cell lung cancer; ovarian cancer;  
XX stomach cancer; breast cancer; colon cancer; bladder cancer; rheumatism;  
XX circulatory disease; hypertension; atherosclerosis; angina; allergy;  
XX inflammatory disease; respiratory disease; asthma; bronchitis;  
XX digestive disease; stomach ulcer; duodenal ulcer; immune disorder;  
XX autoimmune disease; infection; acquired immunodeficiency syndrome; AIDS;  
XX pneumonia; influenza.

XX Homo sapiens.

XX WO200257309-A1.

XX PD 25-JUL-2002.

XX PF 17-JAN-2002; 2002WO-JP000271.

XX PR 18-JAN-2001; 2001JP-00010814.

XX PR 30-MAR-2001; 2001JP-00102558.

XX PA (TAKA) TAKEDA CHEM IND LTD.

XX PI Miwa M, Ito T, Shintani Y, Miyajima N;

XX DR WPI: 2002-538457/57.

XX DR N-PSDB; ABR87584.

XX PT New G-protein coupled receptor protein expressed in human liver for  
design of drugs and reagents for treatment and diagnosis of cancer and  
respiratory metabolic and other diseases.

XX PS Claim 1; Page 89-91; 101pp; Japanese.

XX CC The invention describes a novel G-protein coupled receptor protein  
expressed in human liver. The protein is used in the treatment,  
prevention and diagnosis of central nervous system diseases (such as  
Alzheimer's, anorexia and dementia), metabolic diseases (such as diabetes

CC and hyperlipaemia), cancer (such as non-small cell lung cancer, ovarian  
CC cancer, stomach cancer, breast cancer, colon cancer and bladder cancer),  
CC circulatory diseases (such as hypertension, atherosclerosis and angina),  
CC inflammatory diseases (such as allergy and rheumatism), respiratory  
CC diseases (such as asthma and bronchitis), digestive diseases (such as  
CC stomach ulcer and duodenal ulcer), immune disorders (such as autoimmune  
CC diseases), and infections (such as acquired immunodeficiency syndrome  
CC (AIDS), pneumonia and influenza). This is the amino acid sequence of the  
CC novel G-protein coupled receptor protein described in the invention  
XX

SQ Sequence 318 AA:

Query Match 100.0%; Score 1678; DB 5; Length 318;  
Best Local Similarity 100.0%; Pred. No. 2.6e-177;  
Matches 318; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNGDHVVLGSSVYDCKAIIIVTILLRLVAINGGFITAAAGVWVLRMLPCDKLTV 60  
DB 1 MNGDHVVLGSSVYDCKAIIIVTILLRLVAINGGFITAAAGVWVLRMLPCDKLTV 60  
QY 61 SLGASRFLCQSVVMGKTIYVFLHPMAPYNPVLOFLAFQWDFLNAATLWSSTWLSVFCV 120  
DB 61 SLGASRFLCQSVVMGKTIYVFLHPMAPYNPVLOFLAFQWDFLNAATLWSSTWLSVFCV 120  
QY 121 KIATFHPVFPFVLKHLKSLGMLPMLFSSVGLSFTILLFFIGNHRMYQNTLRNHLQPMNV 180  
DB 121 KIATFHPVFPFVLKHLKSLGMLPMLFSSVGLSFTILLFFIGNHRMYQNTLRNHLQPMNV 180  
QY 181 TGSISRYCEKFFLPLKMITWTMPYAVFICMILLITSLGRHKKALLTTSGRFSPSVQ 240  
DB 181 TGSISRYCEKFFLPLKMITWTMPYAVFICMILLITSLGRHKKALLTTSGRFSPSVQ 240  
QY 241 AHKALLALISFAMLFISYFLSLVFSAGIFPPLDFKFWWESVITYLCAAVHPILLFSN 300  
DB 241 AHKALLALISFAMLFISYFLSLVFSAGIFPPLDFKFWWESVITYLCAAVHPILLFSN 300  
QY 301 CRLRAVLKSRSSRCGTP 318  
DB 301 CRLRAVLKSRSSRCGTP 318

## RESULT 2

ADJ87105 ID ADJ87105 standard; protein; 318 AA.

XX AC ADJ87105;  
XX DT 06-MAY-2004 (first entry)  
XX DE Amino acid sequence of human bitter taste receptor T2R76.  
XX KM Human, bitter taste receptor; T2R76; chromosome 7; bitter taste.  
XX OS Homo sapiens.  
XX PN WO2004011617-A2.  
XX PD 05-FEB-2004.  
XX PF 29-JUL-2003; 2003WO-US023604.  
XX PR 29-JUL-2002; 2002US-0398727P.  
XX PA (SENO-) SENOMYX INC.  
XX PA (ADLER-) ADLER J E.  
XX PA (TANG-) TANG H.  
XX PA (PRON-) PRONIN A.  
XX PA (ZOLL-) ZOLLER M.  
XX PI Adler JE, Tang H, Pronin A, Zoller M;  
XX WPI, 2004-143845/14.  
XX N-PSDB; ADJ87104.  
DR

XX Novel isolated bitter taste receptor, T2R76 polypeptide useful for  
PT identifying modulators of taste perception, or bitter compounds.  
XX  
XX  
XX Claim 5; Page 98-100; 100pp; English.

CC The present sequence represents human bitter taste receptor T2R76. The  
CC human T2R76 gene is located on chromosome 7 in the region 144062692-  
CC 144063648. The reading frame of T2R76 is intronless. T2R76 polypeptides  
CC and polynucleotides are useful for identifying modulators. Such  
CC modulators are useful for modulating bitter taste perception in a  
CC subject. T2R76 agonists can be administered to enhance bitter tastes,  
CC while T2R76 antagonists can be administered to reduce bitter taste.  
XX

SQ Sequence 318 AA:

Query Match 100.0%; Score 1678; DB 8; Length 318;  
Best Local Similarity 100.0%; Pred. No. 2.6e-177;  
Matches 318; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNGDHVVLGSSVYDCKAIIIVTILLRLVAINGGFITAAAGVWVLRMLPCDKLTV 60  
DB 1 MNGDHVVLGSSVYDCKAIIIVTILLRLVAINGGFITAAAGVWVLRMLPCDKLTV 60  
QY 61 SLGASRFLCQSVVMGKTIYVFLHPMAPYNPVLOFLAFQWDFLNAATLWSSTWLSVFCV 120  
DB 61 SLGASRFLCQSVVMGKTIYVFLHPMAPYNPVLOFLAFQWDFLNAATLWSSTWLSVFCV 120  
QY 121 KIATFHPVFPFVLKHLKSLGMLPMLFSSVGLSFTILLFFIGNHRMYQNTLRNHLQPMNV 180  
DB 121 KIATFHPVFPFVLKHLKSLGMLPMLFSSVGLSFTILLFFIGNHRMYQNTLRNHLQPMNV 180  
QY 181 TGSISRYCEKFFLPLKMITWTMPYAVFICMILLITSLGRHKKALLTTSGRFSPSVQ 240  
DB 181 TGSISRYCEKFFLPLKMITWTMPYAVFICMILLITSLGRHKKALLTTSGRFSPSVQ 240  
QY 241 AHKALLALISFAMLFISYFLSLVFSAGIFPPLDFKFWWESVITYLCAAVHPILLFSN 300  
DB 241 AHKALLALISFAMLFISYFLSLVFSAGIFPPLDFKFWWESVITYLCAAVHPILLFSN 300  
QY 301 CRLRAVLKSRSSRCGTP 318  
DB 301 CRLRAVLKSRSSRCGTP 318

## RESULT 3

ADM33335 ID ADM33335 standard; protein; 318 AA.

XX AC ADM33335;  
XX DT 18-NOV-2004 (first entry)  
XX DE Human bitter taste receptor TAS2R60 protein SEQ ID NO:49.  
XX KM human, bitter taste receptor; food.  
XX OS Homo sapiens.  
XX PN WO2004029087-A2.  
XX PD 08-APR-2004.  
XX PF 25-SEP-2003; 2003WO-EP010691.  
XX PR 25-SEP-2002; 2002US-0413298P.  
XX PA (DEER-) DEUT INST ERNAERUNGSPORSCHUNG POTSDAM.  
XX PI Bufer B, Hofmann T, Krautwurst D, Kuhn C, Meyerhof W;  
XX WPI, 2004-305149/28.  
XX N-PSDB; ADM33336.  
DR

XX Novel bitter receptor polynucleotide encoding human TAS2R protein having  
PT bitter substance binding activity, useful for producing nutraceutical or  
PT pharmaceutical compositions comprising antagonists of bitter taste  
receptor activity.  
PS Claim 14; SEQ ID NO 49; 108bp; English.  
XX  
CC The present sequence represents a human bitter taste receptor. Also  
CC described: (1) a polynucleotide encoding a bitter taste receptor (I); (2)  
CC a vector (II) containing (I); (3) a host cell (III) genetically  
CC engineered with (I) or (II); (4) a transgenic non-human animal (IV)  
CC containing (I), (II) and/or (III); (5) a polypeptide (V) having the amino  
CC acid sequence encoded by (I) or obtained by culturing (III) and  
CC recovering polypeptide; (6) an antibody (VI) specifically binding to (V);  
CC (7) a nucleic acid molecule (VII) specifically hybridizing to (I); (8) an  
CC antagonist/inhibitor (VIII) against (V) which is antibody, the  
CC extracellular domain of (V) or its fragment or an inhibiting RNA; (9)  
CC isolating (M2) an antagonist of bitter taste receptor activity; (11) a  
CC foodstuff including human and animal foodstuff, any precursor material or  
CC additive employed in the production of foodstuff comprising (VIII); and  
CC (12) a nutraceutical/pharmaceutical composition comprising (VIII) and an  
CC active agent and optionally a carrier. (III) is useful for producing a  
CC polypeptide encoded by (I), which involves culturing (III) and recovering  
CC the polypeptide encoded by (I). (II) is useful for producing cells  
CC capable of expressing at least one of the bitter taste receptor  
CC polypeptide, which involves genetically cells in vitro with (II), where  
CC the bitter taste receptor polypeptide(s) is(are) encoded by (I). (M1) or  
CC (M2) can be used for producing food or any precursor material or additive  
CC employed in the production of foodstuffs. (M1) or (M2) can also be used  
CC for producing nutraceutical or pharmaceutical compositions. (I), (II),  
CC (VI) or (VIII) can be used for manufacturing a medicament for the  
CC treatment of an abnormally increased or decreased sensitivity towards a  
CC bitter substance. The identified agonist/inhibitor efficiently suppresses  
CC or eliminates bitter tasting components of food and effectively useful in  
CC food industries.  
XX  
SQ Sequence 318 AA:  
Query Match 100.0%; Score 1678; DB 8; Length 318;  
Best Local Similarity 100.0%; Pred. No. 2.6e-177;  
Matches 318; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

AC ABR58013;  
XX  
XX 25-JUL-2003 (first entry)  
DT  
XX  
DE Mouse GI endocrine cell specific GPCR GT2R-m39.  
XX  
XX Chemosensor; G-protein coupled receptor; GPCR; receptor; ion channel;  
KM gastrointestinal tract; taste; endocrine cell.  
XX  
XX Mus musculue.  
OS  
XX  
XX WO2003031604-A1.  
PN  
XX  
PD 17-Apr-2003.  
PD  
XX  
PF 11-OCT-2002; 2002MO-US032664.  
PF  
XX  
XX 12-OCT-2001; 2001US-0328933P.  
PR  
XX  
PA (REGC ) UNIV CALIFORNIA.  
PA (PHLE/) PHLEGER C S W.  
PI  
XX  
PI Walsh JH, Rozenfurt JE, Wu SV;  
DR  
DR WPI; 2003-381713/36.  
DR N-PSDB; ACC44449.  
XX  
PT New nucleic acid encoding a chemosensing G-protein coupled receptor,  
PT useful for identifying chemical sensing receptors and signaling molecules  
PT that allow pharmacological and genetic modulation of taste transduction  
PT pathways.  
XX  
PS Disclosure; Page 63-64; 101bp; English.  
XX  
XX This sequence represents a novel isolated chemosensing G-protein coupled  
CC receptor (GPCR) from the gastrointestinal tract. The encoding nucleic  
CC acid is useful for identifying or isolating chemical sensing receptors  
CC (including taste ion channels) and signaling molecules that would allow  
CC pharmacological and genetic modulation of taste transduction pathways.  
CC The native STC-1 enteroendocrine cells that naturally express GT2R are  
CC useful in identifying modulators of taste receptor-mediated signal  
CC transduction. These cells are also used as models for studying taste-  
CC mediated signal transduction  
XX  
SQ Sequence 312 AA:  
Query Match 57.2%; Score 960; DB 6; Length 312;  
Best Local Similarity 58.8%; Pred. No. 1.4e-97;  
Matches 181; Conservative 46; Mismatches 81; Indels 0; Gaps 0;

## RESULT 5

AAU1389 standard; protein; 307 AA.

AAU1389;

26-MAR-2002 (first entry)

Human T2R71 (hT2R71) polypeptide.

Human; T2R taste GPCR; taste cell-specific G protein-coupled receptor; hT2R71; T2R; bitter taste sensation; taste signaling pathway; taste transduction; food taste masking; drug taste masking.

Homo sapiens.

MO200177676-A1.

18-OCT-2001.

04-APR-2001; 2001MO-US010739.

07-APR-2000; 2000US-0195532P.

13-NOV-2000; 2000US-0247014P.

(SENO-) SENOMYX INC.

Adler JE;

WPI; 2002-017486/02.

N-PSDB; AAS18172.

Novel isolated mammalian taste cell-specific G protein-coupled receptor, T2R, involved in bitter taste sensation, useful for identifying taste modulators that are used to decrease or mask bitter taste of foods or drugs.

Claim 60; Page 75; 103pp; English.

The invention relates to a mammalian taste cell-specific G protein-coupled receptor (GPCR), T2R taste GPCR, involved in bitter taste sensation. The T2R polypeptides and their associated polynucleotides are useful for screening one or more compounds for the presence of taste detectable by a mammal. Modulators of T2R polypeptides (modulators of taste transduction) are useful for pharmacological and genetic modulations of taste signaling pathways. These modulatory compounds are then used in food and pharmaceutical industries to customise taste, e.g., to decrease or mask the bitter taste of foods or drugs. This sequence represents the human T2R71 (hT2R71) polypeptide

Sequence 307 AA;

Query Match 36.3%; Score 609; DB 5; Length 307;

Best Local Similarity 41.9%; Pred. No. 1.3e-58;

Matches 122; Conservative 46; Mismatches 111; Indels 12; Gaps 2;

21 VTLLLLRLVATNGGFTTAAAGVWVLRMLPCDKLVSLGASRFLQSVVMGRTIYV 80

10 VLLFSLSLGLANGFIYVLGKRWLRGRLLPLDMILSLGASRFLQVGTVNFYV 69

81 FLHPMAFPYNPVLOFLAFQWDFLNAATLWSSVYCVKIATFTPVFPMKHLKSGW 140

70 SAQKVEYSGGLGRQFHLHWHFLNSATFWFCGSLVLCVKIANITHSTFLMKRPGW 129

141 LPMMLFSSVGLSFTTILFFIGNHRMYQNYL-----RNHLQPMNVTDGSIIRSYCEKRYLF 195

130 VPMLLGSLVLSIFITLLFFWVNPVYQDFLIRKFSGNMTYKWN-----TRIETYYFP 182

196 PLKMTITMPTAVPFICMILITSLGRRKKALLTTSGRFEPSSQAMIKALLSLPAM 255

183 SLKLVWISIPFSVFLVISMILLNSLRHRTQRMOHGSHLQDPSTQATRALKSLISFLIL 242

QY 256 FISYFLSVFSAAGIPPLDFKRWVESVIYCAAVHPITLLPSNCRRAV 306  
DB 243 YALSFSLIIDAKFISMQNDFFYWPQIAVYLCISVHPITLLFSNKLRSV 293

## RESULT 6

ABP95935 standard; protein; 307 AA.

ABP95935;

06-MAR-2003 (first entry)

Human GPCR polypeptide SEQ ID NO 680.

Human; GPCR; G protein coupled receptor; signal transduction; olfactory; drug development; gustatory; taste; fragrance; receptor.

Homo sapiens.

MO200216548-A2.

28-FEB-2002.

30-JUL-2001; 2001MO-IB001446.

04-AUG-2000; 2000JP-00237818.

13-FEB-2001; 2001JP-00034434.

(NISC-) JAPAN SCI &amp; TECHNOLOGY CORP.

Haga T, Takeda S, Mitaku S;

WPI; 2002-304118/34.

N-PSDB; ABZ43209.

Database global search for G protein-coupled receptors, proteins and encoded genes for studying in vivo signal transduction mechanism and identifying targets for drug development.

Claim 10; SEQ ID NO 680; 97pp + Sequence Listing; Japanese.

The invention relates to a method for screening G protein-coupled receptor (GPCR) genes (ABZ42870-ABZ43216) and/or GPCR proteins (ABP95596-ABP95942) by extracting open-reading frames containing 6-8 transmembrane domains with 250-1000 amino acid residues to give a gene homologous with a known GPCR gene. The receptor proteins and encoded genes are useful for studying in vivo signal transduction mechanism and identifying targets for drug development e.g. based on olfactory and gustatory receptors in form of agonists and antagonists by screening intrinsic and extrinsic CC ligands as bitter taste inhibitors, taste enhancers and fragrance improvers. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

Sequence 307 AA;

Query Match 36.3%; Score 609; DB 5; Length 307;

Best Local Similarity 41.9%; Pred. No. 1.3e-58;

Matches 122; Conservative 46; Mismatches 111; Indels 12; Gaps 2;

21 VTLLLLRLVATNGGFTTAAAGVWVLRMLPCDKLVSLGASRFLQSVVMGRTIYV 80

10 VLLFSLSLGLANGFIYVLGKRWLRGRLLPLDMILSLGASRFLQVGTVNFYV 69

81 FLHPMAFPYNPVLOFLAFQWDFLNAATLWSSVYCVKIATFTPVFPMKHLKSGW 140

70 SAQKVEYSGGLGRQFHLHWHFLNSATFWFCGSLVLCVKIANITHSTFLMKRPGW 129

141 LPMMLFSSVGLSFTTILFFIGNHRMYQNYL-----RNHLQPMNVTDGSIIRSYCEKRYLF 195

130 VPMLLGSLVLSIFITLLFFWVNPVYQDFLIRKFSGNMTYKWN-----TRIETYYFP 182



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OM protein - protein search, using sw model

Run on: February 4, 2005, 16:58:16 ; Search time 22 Seconds  
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1079.018 Million cell updates/sec

Title: US-10-628-464-2

Perfect score: 1678

Sequence: 1 MNGDHVVLGSSVTDKKAIL.....SNCRRLAVLKRRSSRCGTP 318

Scoring table:

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Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

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Maximum Match 100%

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- 4: /cgn2\_6/ptodata/1/1aa/6B.COMB.pep:\*
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- 6: /cgn2\_6/ptodata/1/1aa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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5	378.5	22.6	318	4	US-09-949-016-9253
6	359	21.4	312	4	US-09-393-634-51
7	356	21.2	299	4	US-09-393-634-5
8	337.5	20.1	309	4	US-09-393-634-49
9	336	20.0	299	4	US-09-393-634-35
10	332.5	19.8	316	4	US-09-393-634-39
11	332.5	19.8	316	4	US-09-949-016-8207
12	329.5	19.6	302	4	US-09-393-634-37
13	319.5	19.0	335	4	US-09-393-634-1
14	304	18.1	300	4	US-09-393-634-58
15	293	17.5	299	4	US-09-393-634-43
16	293	17.5	299	4	US-09-949-016-6942
17	293	17.5	299	4	US-09-949-016-8156
18	283	16.9	300	4	US-09-393-634-17
19	279	16.3	300	4	US-09-393-634-19
20	273.5	15.9	310	4	US-09-393-634-53
21	266	15.8	299	4	US-09-393-634-41
22	264.5	15.1	300	4	US-09-393-634-47
23	254	14.4	315	4	US-09-393-634-56
24	240.5	14.3	333	4	US-09-393-634-3
25	231.5	13.8	317	4	US-09-393-634-60
26	231.5	13.8	266	4	US-09-393-634-15
27	212.5	12.7	266	4	US-09-393-634-15

28	200.5	11.9	224	4	US-09-393-634-9	Sequence 9, Appl
29	152.5	9.1	209	4	US-09-393-634-13	Sequence 13, Appl
30	151.5	9.0	121	4	US-09-393-634-70	Sequence 70, Appl
31	145.5	8.7	173	4	US-09-393-634-23	Sequence 23, Appl
32	140.5	8.4	180	4	US-09-393-634-33	Sequence 33, Appl
33	134	8.0	115	4	US-09-393-634-27	Sequence 27, Appl
34	131	7.8	144	4	US-09-393-634-66	Sequence 66, Appl
35	129.5	7.7	155	4	US-09-393-634-21	Sequence 21, Appl
36	123.5	7.4	129	4	US-09-393-634-72	Sequence 72, Appl
37	121	7.2	126	4	US-09-393-634-31	Sequence 31, Appl
38	120	7.2	355	4	US-09-170-496D-2	Sequence 2, Appl
39	120	7.2	355	4	US-09-170-496D-164	Sequence 164, App
40	117.5	7.0	450	4	US-09-721-870-16	Sequence 16, Appl
41	116.5	6.9	359	2	US-08-467-568-13	Sequence 27, Appl
42	116.5	6.9	359	2	US-08-748-485-4	Sequence 13, Appl
43	116.5	6.9	359	2	US-08-103-170-2	Sequence 4, Appl
44	116.5	6.9	359	2	US-09-030-582-13	Sequence 2, Appl
45	116.5	6.9	359	3	US-09-171-456-19	Sequence 13, Appl
						Sequence 19, Appl

## ALIGNMENTS

```
RESULT 1
US-09-949-016-8213
; Sequence 8213, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949, 016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241, 755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237, 768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231, 498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8213
; LENGTH: 291
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-8213

Query Match      24.8% Score 416; DB 4; Length 291;
Best Local Similarity 32.1%; Pred. No. 4.4e-32;
Matches 94; Conservative 55; Mismatches 134; Indels 10; Gaps 3;

QY      18 IIVTLLRLRLVAINGFTLALGVEWVLRMLPCDLVSLGASRCLQSVWGKT 77
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      8 VFMIITVLESLLTIYQSSILVAVLGREMLQVRLMPVDMLISLGSRCLQMASLNN 67
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      78 IYVFLHPMAPVNPVIOFLAFQMDPLNATLWSLVSFYCYXIAITFTTPVFMKHL 137
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      68 FCSY-----FNLNVVLCNLTITWTFEFNILTFWINSILTYFYCYKVSFTTHIFLMWRRI 122
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      138 SGLPMMVLPSVGLSFTTILTFPIGNHMYQNTLRNHLQPMWNTGSIYSCKKFLFPL 197
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      123 LRFPMLIGSLMLTTCVTIIPSAIGNYIQIQLTMEHLPRNSTVTDKLENFQ--YQFA 180
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      198 KMTWTMPVAFPICMILITSLGRKRALTTSGFRSPVOAHTKALIALSPAMLFT 257
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      181 HTAAVYIPFLFLASTIFLMASL---TKQGHSTHCNCPMSKAHFTALRSALVFLVFT 237
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      258 SYFLSLVFSAGLFPPLDFKFWWESVIYCAAVPIILFNSCRRLPAVLKSR 310
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      238 SYFLTLITITIGTLFDKRCWLMWEAFVYAFILMHSITSLMSSPTLKRLKXK 290
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
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RESULT 2  
US-09-393-634-64  
Sequence 64, Application US/09393634  
Patent No. 6558910  
GENERAL INFORMATION:  
APPLICANT: Zuker, Charles S.  
APPLICANT: Adler, Jon Elliot  
APPLICANT: Ryba, Nick  
APPLICANT: Mueller, Ken  
APPLICANT: Hoon, Mark  
APPLICANT: The Regents of the University of California  
APPLICANT: The Government of the United States of America  
APPLICANT: as represented by the Secretary of the  
Department of Health and Human Services  
TITLE OF INVENTION: SF, a No. 6558910el Family of Taste Receptors  
FILE REFERENCE: 02307E-098000US  
CURRENT APPLICATION NUMBER: US/09/393,634  
CURRENT FILING DATE: 1999-09-10  
NUMBER OF SEQ ID NOS: 92  
SOFTWARE: Patent In Ver. 2.1  
LENGTH: 291  
SEQ ID NO 64  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: human GR16  
US-09-393-634-64

Query Match  
Best Local Similarity 24.3%; Score 408; DB 4; Length 291;  
Best Local Similarity 31.7%; Pred. No. 2,6e-31;  
Matches 93; Conservative 55; Mismatches 135; Indels 10; Gaps 3;

18 IIVTLLRLVAIAAGNGFITAAAGVWVLRMLPCDCLVSLGASRFLQSVVMGKT 77  
8 VFEMITVLESITIVQSSLIYAVLGREWLQVRRLPVMILISGISRFLQSMASMLNN 67  
78 IYVFLHPMAFPYNPVLOFLAFQWDFLNAATLSSVYCYCKIATFTHPVFMKHL 137  
68 FCSY-----FNINLVYCNLTITWEPFNILTFPLNSLTIVFYCIKVSFTHHIFLMRWRI 122  
138 SGWLPWMLFSSVGLSFTTILFFIGNHRYQNYLRNHLQPMNVTDGSIKSYCEKFLPPL 197  
123 LRLFPWILGSLMITCVTIIPSAIGNYIOQLTMEHLPRNSTVTDKLENFHO--YQFOA 180  
198 KMTWMPRAVFFICMILITSLGRRKKALLTSGFRPSVOAHIKALLLSPFAMLF 257  
181 HTVALVIPFLPLASTIFLMAQL--TKQIQHSTGHCHNPSMKARFTALRSALVLFVFT 237  
258 SYFLSLVFSAGIFPPLDFKFWWESVLYLCAAVHPILILFNSCRLRAVLKSR 310  
238 SYFLTILITITIGTLFPDKRCWLWMEAFVAFILMHSSTLMSPTLKRLKKGK 290

RESULT 3  
US-09-949-016-6919  
Sequence 6919, Application US/09949016  
Patent No. 6812339  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: CLO01307  
CURRENT APPLICATION NUMBER: US/09/949,016  
CURRENT FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 6919

LENGTH: 291  
TYPE: PRT  
ORGANISM: Human  
US-09-949-016-6919

Query Match  
Best Local Similarity 24.3%; Score 408; DB 4; Length 291;  
Best Local Similarity 31.7%; Pred. No. 2,6e-31;  
Matches 93; Conservative 55; Mismatches 135; Indels 10; Gaps 3;

18 IIVTLLRLVAIAAGNGFITAAAGVWVLRMLPCDCLVSLGASRFLQSVVMGKT 77  
8 VFEMITVLESITIVQSSLIYAVLGREWLQVRRLPVMILISGISRFLQSMASMLNN 67  
78 IYVFLHPMAFPYNPVLOFLAFQWDFLNAATLSSVYCYCKIATFTHPVFMKHL 137  
68 FCSY-----FNINLVYCNLTITWEPFNILTFPLNSLTIVFYCIKVSFTHHIFLMRWRI 122  
138 SGWLPWMLFSSVGLSFTTILFFIGNHRYQNYLRNHLQPMNVTDGSIKSYCEKFLPPL 197  
123 LRLFPWILGSLMITCVTIIPSAIGNYIOQLTMEHLPRNSTVTDKLENFHO--YQFOA 180  
198 KMTWMPRAVFFICMILITSLGRRKKALLTSGFRPSVOAHIKALLLSPFAMLF 257  
181 HTVALVIPFLPLASTIFLMAQL--TKQIQHSTGHCHNPSMKARFTALRSALVLFVFT 237  
258 SYFLSLVFSAGIFPPLDFKFWWESVLYLCAAVHPILILFNSCRLRAVLKSR 310  
238 SYFLTILITITIGTLFPDKRCWLWMEAFVAFILMHSSTLMSPTLKRLKKGK 290

RESULT 4  
US-09-393-634-47  
Sequence 47, Application US/09393634  
Patent No. 6558910  
GENERAL INFORMATION:  
APPLICANT: Zuker, Charles S.  
APPLICANT: Adler, Jon Elliot  
APPLICANT: Ryba, Nick  
APPLICANT: Mueller, Ken  
APPLICANT: Hoon, Mark  
APPLICANT: The Regents of the University of California  
APPLICANT: The Government of the United States of America  
APPLICANT: as represented by the Secretary of the  
Department of Health and Human Services  
TITLE OF INVENTION: SF, a No. 6558910el Family of Taste Receptors  
FILE REFERENCE: 02307E-098000US  
CURRENT APPLICATION NUMBER: US/09/393,634  
CURRENT FILING DATE: 1999-09-10  
NUMBER OF SEQ ID NOS: 92  
SOFTWARE: Patent In Ver. 2.1  
LENGTH: 318  
SEQ ID NO 47  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: human GR07  
US-09-393-634-47

Query Match  
Best Local Similarity 22.6%; Score 378.5; DB 4; Length 318;  
Best Local Similarity 29.4%; Pred. No. 2e-28;  
Matches 91; Conservative 60; Mismatches 135; Indels 23; Gaps 5;

22 TILLRL-----VLAAGNGFITAAAGVWVLRMLPCDCLVSLGASRFLQSVVMGKT 77  
7 TLLFLAVGEFVGLIGNAFIGLVNCDWVKRKRKIASIDLITSLAISICLLCYILLDC 66  
78 IYVFLHPMAFPYNPVLOFLAFQWDFLNAATLSSVYCYCKIATFTHPVFMKHL 137  
67 FLIVLYPDVYATGKEMRIIDFFWTLNHSIFATCLSIYFPGKGNFPHPLFMMWKRI 126  
138 SGWLPWMLFSSVGLSFTTILF--FIGNHRNYQNYLRNHLQPMNVTDGSIKSYCEKFL 194  
127 DRVISWILGCVLVSFISLPATENLMDFRFCVAKRKTNLTWSCRVAKTQHAATKFL 186

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 4, 2005, 17:02:31 ; Search time 132 Seconds

(without alignments)  
784.647 Million cell updates/sec

Title: US-10-628-464-2

Perfect score: 1678  
Sequence: 1 MNGDHWLVGSSVTDKAIL.....SNCRILAVLKRRSSRCGTP 318

Scoring table:

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Gapop 10.0 , Gapext 0.5

Searched: 1373511 seqs, 325702437 residues

Total number of hits satisfying chosen parameters: 1373511

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:\*

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2: /cgn2\_6/ptodata/2/pubppaa/PCT\_NEW\_PUB.pep:\*

3: /cgn2\_6/ptodata/2/pubppaa/US06\_NEW\_PUB.pep:\*

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17: /cgn2\_6/ptodata/2/pubppaa/US20\_NEW\_PUB.pep:\*

18: /cgn2\_6/ptodata/2/pubppaa/US21\_NEW\_PUB.pep:\*

19: /cgn2\_6/ptodata/2/pubppaa/US22\_NEW\_PUB.pep:\*

20: /cgn2\_6/ptodata/2/pubppaa/US23\_NEW\_PUB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1678	100.0	318	16	US-10-628-464-2
2	609	36.3	307	9	US-09-825-882-18
3	609	36.3	307	14	US-10-017-161-1786
4	609	36.3	307	15	US-10-292-798-1442
5	609	36.3	307	10	US-10-343-650A-680
6	597.5	35.6	308	15	US-09-510-332-155
7	589.5	35.1	308	10	US-09-510-332-99
8	408	24.3	291	9	US-09-393-634-64
9	408	24.3	291	10	US-09-510-332-30
10	408	24.3	291	14	US-10-383-982-64
11	378.5	22.6	318	9	US-10-364-861-64
12	378.5	22.6	318	9	US-09-393-634-47
13	378.5	22.6	318	10	US-09-510-332-13

14	378.5	22.6	318	14	US-10-383-982-47	Sequence 47, Appl1
15	378.5	22.6	318	15	US-10-364-861-47	Sequence 47, Appl1
16	371	22.1	299	10	US-09-510-332-139	Sequence 139, Appl
17	359	21.4	312	9	US-09-393-634-51	Sequence 51, Appl1
18	359	21.4	312	9	US-09-510-332-17	Sequence 17, Appl1
19	359	21.4	312	10	US-10-383-982-51	Sequence 51, Appl1
20	359	21.4	312	15	US-10-364-861-51	Sequence 51, Appl1
21	356	21.2	299	9	US-09-393-634-51	Sequence 51, Appl1
22	356	21.2	299	10	US-09-510-332-81	Sequence 81, Appl1
23	356	21.2	299	14	US-10-383-982-5	Sequence 5, Appl1
24	356	21.2	299	15	US-10-364-861-5	Sequence 5, Appl1
25	344.5	20.5	297	10	US-09-510-332-87	Sequence 87, Appl1
26	339	20.2	321	9	US-09-825-882-4	Sequence 4, Appl1
27	339	20.2	331	15	US-10-292-798-1732	Sequence 1732, Ap
28	339	20.2	331	14	US-10-017-161-2086	Sequence 2086, Ap
29	339	20.2	338	14	US-10-017-161-2140	Sequence 2140, Ap
30	339	20.2	338	15	US-10-292-798-1786	Sequence 1786, Ap
31	339	20.2	338	15	US-10-343-650A-676	Sequence 676, App
32	338	20.1	338	15	US-10-343-650A-678	Sequence 678, App
33	337.5	20.1	309	9	US-09-393-634-49	Sequence 49, Appl1
34	337.5	20.1	309	10	US-09-510-332-15	Sequence 15, Appl1
35	337.5	20.1	309	14	US-10-383-982-49	Sequence 49, Appl1
36	337.5	20.1	309	15	US-10-364-861-49	Sequence 49, Appl1
37	336.5	20.1	312	10	US-09-510-332-162	Sequence 162, App
38	336	20.0	299	9	US-09-393-634-35	Sequence 35, Appl1
39	336	20.0	299	10	US-09-510-332-35	Sequence 35, Appl1
40	336	20.0	299	14	US-10-383-982-35	Sequence 35, Appl1
41	336	20.0	299	15	US-10-364-861-35	Sequence 35, Appl1
42	332.5	19.8	316	9	US-09-393-634-39	Sequence 39, Appl1
43	332.5	19.8	316	10	US-09-510-332-5	Sequence 5, Appl1
44	332.5	19.8	316	14	US-10-383-982-39	Sequence 39, Appl1
45	332.5	19.8	316	15	US-10-364-861-39	Sequence 39, Appl1

#### ALIGNMENTS

RESULT 1

US-10-628-464-2

Sequence 2, Application US/10628464

Publication No. US2004012134A1

GENERAL INFORMATION:

APPLICANT: ADLER, JON ELLIOT

APPLICANT: TANG, HUIXIAN

APPLICANT: PRONIN, ALEXEY

TITLE OF INVENTION: IDENTIFICATION OF A NOVEL BITTER TASTE RECEPTOR, T2R76

FILE REFERENCE: 100337.54260US

CURRENT APPLICATION NUMBER: US/10/628,464

CURRENT FILING DATE: 2003-07-29

NUMBER OF SEQ ID NOS: 2

SOFTWARE: Patentin Ver. 3.2

SEQ ID NO 2

LENGTH: 318

TYPE: PRT

ORGANISM: Homo sapiens

US-10-628-464-2

Query Match	100.0%	Score 1678;	DB 16;	Length 318;
Best Local Similarity	100.0%	Pred. No. 1.8e-144;		
Matches 318;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MNGDHWLVGSSVTDKAILVTLLRLVAINGRFTALGVENWLRMLPCDGLV	60	
DB	1	MNGDHWLVGSSVTDKAILVTLLRLVAINGRFTALGVENWLRMLPCDGLV	60	
QY	61	SLGSRFCLOSVMGKTIYVFLHPMAFPYVLOFLAFQWDPLNAATLMSSTLVSFVCV	120	
DB	61	SLGSRFCLOSVMGKTIYVFLHPMAFPYVLOFLAFQWDPLNAATLMSSTLVSFVCV	120	
QY	121	KIATFTPVFPMWKHKLISGWLPMMLFSSVGLSFTTTLFTGNHRMYONTLRNHLQPMNV	180	
DB	121	KIATFTPVFPMWKHKLISGWLPMMLFSSVGLSFTTTLFTGNHRMYONTLRNHLQPMNV	180	

QY 181 TGDINSYCEKFLPFLKMTWMTPTAVFICMILLITSGRRKKALLTSGPREPSVQ 240  
| : : : : :  
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QY 241 AHKALLALISFPMFLFSYFLSVFSAGIFPPLDFKFWMESVIYLCAAVHPITLLFSN 300  
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DB 241 AHKALLALISFPMFLFSYFLSVFSAGIFPPLDFKFWMESVIYLCAAVHPITLLFSN 300  
QY 301 CRLRAVLKRRSSRCGTP 318  
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DB 301 CRLRAVLKRRSSRCGTP 318

RESULT 2  
US-09-825-882-18  
; Sequence 18; Application US/09825882  
; Patent No. US20020094551A1  
; GENERAL INFORMATION:  
; APPLICANT: ADLER, JON ELLIOT  
; TITLE OF INVENTION: T2R TASTE RECEPTORS AND GENES ENCODING SAME  
; FILE REFERENCE: 078003/0279152/RXT  
; CURRENT APPLICATION NUMBER: US/09/825,882  
; CURRENT FILING DATE: 2001-04-05  
; PRIOR APPLICATION NUMBER: 60/195,532  
; PRIOR FILING DATE: 2000-04-07  
; PRIOR APPLICATION NUMBER: 60/247,014  
; PRIOR FILING DATE: 2000-11-13  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 18  
; LENGTH: 307  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-825-882-18

Query Match 36.3%; Score 609; DB 9; Length 307;  
Best Local Similarity 41.9%; Pred. No. 3.5e-47;  
Matches 122; Conservative 46; Mismatches 111; Indels 12; Gaps 2;  
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| : : : : :  
DB 10 VLLFSLSLGIAANGFIVLVGREWLRGRLLPDMILISIGASRFCLQVGTVNFYV 69  
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| : : : : :  
DB 70 SAQKVEYSGGLGRQFHLHWHFINSATFWFCMSLVSFVKIANITHTSTFLMKMFPGM 129  
QY 141 LPMMLSSVGLSFTTILFPIGNHRMYONYL-----RNHLQPMWVTGDSIRSYCEKFLYF 195  
| : : : : :  
DB 130 VPMLLGSLVLSIFITLLFFWVNPVYQEFLLIRKFSGNMTYKWN-----TTEITYYPP 182  
QY 196 PLKMTWMTPTAVFICMILLITSGRRKKALLTSGPREPSVQAHKALLALISFPMFL 255  
| : : : : :  
DB 183 SLKLVWISIPFSVFLVSIMLLNSLRHTQRQMHNSLQDPSQTQHTALSLISFLIL 242  
QY 256 FISYFLSVLSAAGIFPPLDFKFWMESVIYLCAAVHPITLLFSNCRRLAV 306  
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RESULT 3  
US-10-017-161-1786  
; Sequence 1786; Application US/10017161  
; Publication No. US20030143668A1  
; GENERAL INFORMATION:  
; APPLICANT: SUMA, MAKIKO  
; APPLICANT: ASAI, KIYOSHI  
; APPLICANT: AKIYAMA, YUTAKA  
; APPLICANT: AUBURATANI, HIROYUKI  
; TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS  
; FILE REFERENCE: 084335/0152  
; CURRENT APPLICATION NUMBER: US/10/017,161  
; CURRENT FILING DATE: 2002-12-18

; PRIOR APPLICATION NUMBER: JP 2001/246789  
; PRIOR FILING DATE: 2001-06-18  
; NUMBER OF SEQ ID NOS: 2430  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1786  
; LENGTH: 307  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-017-161-1786

Query Match 36.3%; Score 609; DB 14; Length 307;  
Best Local Similarity 41.9%; Pred. No. 3.5e-47;  
Matches 122; Conservative 46; Mismatches 111; Indels 12; Gaps 2;  
QY 21 VTILLRLVAIAGNGFITPAALGVEWVLRMLPCDKLVSIGASRFCLQSVMGKTIYV 80  
| : : : : :  
DB 10 VLLFSLSLGIAANGFIVLVGREWLRGRLLPDMILISIGASRFCLQVGTVNFYV 69  
QY 81 FLHPMAFPYNPVLOFLAFOQDFLNAATLWSSTWLSVFCVKIATFTHPVFWLKHLSGM 140  
| : : : : :  
DB 70 SAQKVEYSGGLGRQFHLHWHFINSATFWFCMSLVSFVKIANITHTSTFLMKMFPGM 129  
QY 141 LPMMLSSVGLSFTTILFPIGNHRMYONYL-----RNHLQPMWVTGDSIRSYCEKFLYF 195  
| : : : : :  
DB 130 VPMLLGSLVLSIFITLLFFWVNPVYQEFLLIRKFSGNMTYKWN-----TTEITYYPP 182  
QY 196 PLKMTWMTPTAVFICMILLITSGRRKKALLTSGPREPSVQAHKALLALISFPMFL 255  
| : : : : :  
DB 183 SLKLVWISIPFSVFLVSIMLLNSLRHTQRQMHNSLQDPSQTQHTALSLISFLIL 242  
QY 256 FISYFLSVLSAAGIFPPLDFKFWMESVIYLCAAVHPITLLFSNCRRLAV 306  
| : : : : :  
DB 243 YALSFSLIITDAKFIQMNDPYWPMQIAYVLCISVHPILIFSMLKLRSV 293

RESULT 4  
US-10-292-798-1442  
; Sequence 1442; Application US/10292798  
; Publication No. US20030235833A1  
; GENERAL INFORMATION:  
; APPLICANT: SUMA, MAKIKO  
; APPLICANT: ASAI, KIYOSHI  
; APPLICANT: AKIYAMA, YUTAKA  
; APPLICANT: AUBURATANI, HIROYUKI  
; TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS  
; FILE REFERENCE: 084335/166  
; CURRENT APPLICATION NUMBER: US/10/292,798  
; CURRENT FILING DATE: 2002-11-13  
; PRIOR APPLICATION NUMBER: 10/017,161  
; PRIOR FILING DATE: 2001-12-18  
; PRIOR APPLICATION NUMBER: JP 2001-246789  
; PRIOR FILING DATE: 2001-06-18  
; NUMBER OF SEQ ID NOS: 2070  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1442  
; LENGTH: 307  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-292-798-1442

Query Match 36.3%; Score 609; DB 15; Length 307;  
Best Local Similarity 41.9%; Pred. No. 3.5e-47;  
Matches 122; Conservative 46; Mismatches 111; Indels 12; Gaps 2;  
QY 21 VTILLRLVAIAGNGFITPAALGVEWVLRMLPCDKLVSIGASRFCLQSVMGKTIYV 80  
| : : : : :  
DB 10 VLLFSLSLGIAANGFIVLVGREWLRGRLLPDMILISIGASRFCLQVGTVNFYV 69  
QY 81 FLHPMAFPYNPVLOFLAFOQDFLNAATLWSSTWLSVFCVKIATFTHPVFWLKHLSGM 140  
| : : : : :  
DB 70 SAQKVEYSGGLGRQFHLHWHFINSATFWFCMSLVSFVKIANITHTSTFLMKMFPGM 129  
QY 141 LPMMLSSVGLSFTTILFPIGNHRMYONYL-----RNHLQPMWVTGDSIRSYCEKFLYF 195





GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 4, 2005, 16:58:16 ; Search time 63 Seconds

(without alignments)  
2584.781 Million cell updates/sec

Title: US-10-628-464-2

Perfect score: 1678

Sequence: 1 MNGDHWLGSSTVDKKAIL.....SNCRLRAVLKRRSRSGCTP 318

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1678	100.0	318	1 TR60 HUMAN	P59551 homo sapien
2	1638	97.6	318	2 O646T5	O646T5 pan troglod
3	1630	97.1	318	2 O646D0	O646D0 pan paniscu
4	1622	96.7	318	2 O645Z0	O645Z0 gorilla gor
5	1514	90.2	318	2 O645U7	O645U7 pongo pygma
6	1480	88.2	318	2 O645S2	O645S2 macaca mula
7	960	57.2	312	1 TR35 MOUSE	O7TQ97 mus musculu
8	953	56.8	321	2 O67BE2	O67BE2 rattus norv
9	608	36.2	307	1 TR41 HUMAN	P59536 homo sapien
10	607	36.2	307	2 O646B2	O646B2 pan troglod
11	600	35.8	307	2 O646C7	O646C7 pan paniscu
12	597.5	35.6	308	1 T2RC MOUSE	P59532 mus musculu
13	597.5	35.6	308	2 O7M7D4	O7M7D4 mus musculu
14	595	35.5	307	2 O645Y3	O645Y3 gorilla gor
15	589.5	35.1	308	1 T2RC RAT	O645Y3 rattus norv
16	580	34.6	307	2 O645U6	O645U6 pongo pygma
17	560	33.4	307	2 O645S8	O645S8 macaca mula
18	560	33.4	307	2 O646F3	O646F3 papio hamad
19	431	25.7	291	2 O645U1	O645U1 pongo pygma
20	427	25.4	298	1 TR34 MOUSE	O7TQ97 mus musculu
21	425	25.3	294	2 O67BE3	O67BE3 rattus norv
22	423	25.2	291	2 O646B3	O646B3 pan troglod
23	421	25.1	291	2 O645Y4	O645Y4 gorilla gor
24	421	25.1	291	2 O646B7	O646B7 papio hamad
25	419	25.0	291	2 O646A6	O646A6 pan troglod
26	418.5	24.9	329	2 O646T1	O646T1 pan paniscu
27	418.5	24.9	329	2 O67BE7	O67BE7 rattus norv
28	416	24.8	291	2 O645W1	O645W1 homo sapien
29	415	24.7	291	2 O645S3	O645S3 macaca mula
30	408	24.3	291	1 T2RG HUMAN	O9NYV3 homo sapien
31	402.5	24.0	293	1 TR43 MOUSE	O7TQ97 mus musculu

32	379.5	22.6	318	2 O645T7	O645T7 macaca mula
33	378.5	22.6	318	1 T2R7 HUMAN	O9NYV3 homo sapien
34	378.5	22.6	319	2 O646C4	O646C4 pan troglod
35	378.5	22.6	319	2 O646D6	O646D6 pan paniscu
36	377.5	22.5	317	2 O646F6	O646F6 papio hamad
37	376.5	22.4	318	2 O646A2	O646A2 gorilla gor
38	374.5	22.3	318	2 O645V8	P59529 mus musculu
39	371	22.1	299	1 T2R3 MOUSE	O7M728 mus musculu
40	371	22.1	299	2 O7M728	O7M728 mus musculu
41	362	21.6	311	2 O645T0	O645T0 macaca mula
42	359	21.4	312	1 T2R9 HUMAN	O9NYV1 homo sapien
43	358	21.3	312	2 O645W9	O645W9 homo sapien
44	357	21.3	299	1 T2R1 CERAE	O8MJU6 cercopithec
45	357	21.3	311	2 O646G5	O646G5 papio hamad

#### ALIGNMENTS

RESULT 1  
TR60 HUMAN STANDARD; PRT; 318 AA.  
ID TR60\_HUMAN  
AC P59551; Q7RTR7;  
DT 10-OCT-2003 (Rel. 42, Created)  
DT 10-OCT-2003 (Rel. 42, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Taste receptor type 2 member 60 (T2R60).  
GN Name=TAS2R60;  
OS Homo sapiens (human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22471936; PubMed=12584440; DOI=10.1159/000068546;  
RA Conte C., Ebelling M., Marcuz A., Nef P., Andres-Barguin P. J.;  
RT "Identification and characterization of human taste receptor genes  
belonging to the TAS2R family.";  
RL Cytogenet. Genome Res. 98:45-53(2002).  
RN [2]  
RP REVIEW.  
RX MEDLINE=2213574; PubMed=1213982; DOI=10.1016/S0959-4388(02)00345-8;  
RA Montmayeur J.-P., Matsunami H.;  
RT "Receptors for bitter and sweet taste.";  
RL Curr. Opin. Neurobiol. 12:366-371(2002).  
RN [3]  
RP REVIEW.  
RX MEDLINE=21634924; PubMed=11696554; DOI=10.1074/jbc.R100054200;  
RA Margolske R. F.;  
RT "Molecular mechanisms of bitter and sweet taste transduction.";  
RL J. Biol. Chem. 277:1-4(2002).  
RN [4]  
RP REVIEW.  
RX MEDLINE=22469025; PubMed=12581520; DOI=10.1016/S0092-8674(03)00071-0;  
RA Zhang Y., Hoon M.A., Chandrasekar J., Mueller K.L., Cook B., Wu D.,  
Zaker C.S., Ryba N.J.;  
RT "Coding of sweet, bitter, and umami tastes: different receptor cells  
sharing similar signaling pathways.";  
RL Cell 112:293-301(2003).  
RN [5]  
RP PHYLOGENETIC ANALYSIS.  
RX MEDLINE=2258047; PubMed=12679530; DOI=10.1093/molbev/mg083;  
RA Shi P., Zhang Y., Yang H., Zhang Y. P.;  
RT "Adaptive diversification of bitter taste receptor genes in Mammalian  
evolution.";  
RL Mol. Biol. Evol. 20:805-814(2003).  
CC -1- FUNCTION: Receptor that may play a role in the perception of  
bitterness and is gustducin-linked. May play a role in sensing the  
chemical composition of the gastrointestinal content. The activity  
of this receptor may stimulate alpha gustducin, mediate PLC-beta-2  
activation and lead to the gating of TRPM5 (By similarity).  
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -1- TISSUE SPECIFICITY: Expressed in subsets of taste receptor cells

CC of the tongue and exclusively in gustducin-positive cells.  
CC -1- MISCELLANEOUS: Most taste cells may be activated by a limited  
CC number of bitter compounds; individual taste cells can  
CC discriminate among bitter stimuli.  
CC -1- SIMILARITY: Belongs to the G-protein coupled receptor T2R family.  
CC  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.1sb-sib.ch/announce/>  
CC or send an email to [license@1sb-sib.ch](mailto:license@1sb-sib.ch)).  
CC  
CC EMBL; AY114094; AAM63544.1; -;  
CC EMBL; BK001100; DAA01207.1; -;  
CC Genew; HGNC:20639; TAS2R60.  
CC InterPro; IPR007960; TAS2\_Recept.  
CC  
CC G-protein coupled receptor; Receptor; Transmembrane.  
CC FT DOMAIN 1 7  
CC FT TRANSMEM 28 7  
CC FT DOMAIN 29 40  
CC FT TRANSMEM 41 61  
CC FT DOMAIN 62 88  
CC FT TRANSMEM 89 109  
CC FT DOMAIN 110 128  
CC FT TRANSMEM 129 149  
CC FT DOMAIN 150 183  
CC FT TRANSMEM 184 204  
CC FT DOMAIN 205 234  
CC FT TRANSMEM 235 255  
CC FT DOMAIN 256 264  
CC FT TRANSMEM 265 285  
CC FT CARBOHYD 179 179  
CC FT SEQUENCE 318 AA; 36336 MW; DEDABIIC81017648 CRC64;  
CC  
CC Query Match 100.0%; Score 1678; DB 1; Length 318;  
CC Best Local Similarity 100.0%; Pred. No. 4.1e-116;  
CC Matches 318; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
CC  
CC QY 1 MNGDHWLVGSSVTDKKAIIIVTILLRLVAIAGNGFTTAAIGVWVLRMLPCDKLIV 60  
CC DB 1 MNGDHWLVGSSVTDKKAIIIVTILLRLVAIAGNGFTTAAIGVWVLRMLPCDKLIV 60  
CC  
CC QY 61 SLGASRFCLQSVVMGKTIYVFLHPMAFPYNPVLOFLAFQWDFLNAATLWSSTWLSVFCV 120  
CC DB 61 SLGASRFCLQSVVMGKTIYVFLHPMAFPYNPVLOFLAFQWDFLNAATLWSSTWLSVFCV 120  
CC  
CC QY 121 KIATFTHPVFPMVKHKLKSGMLPWWLFFSVGLSFTTILFFIGNHMYQNYLRNHLQPMNV 180  
CC DB 121 KIATFTHPVFPMVKHKLKSGMLPWWLFFSVGLSFTTILFFIGNHMYQNYLRNHLQPMNV 180  
CC  
CC QY 181 TGSINSYCEKFFLPKMTITWPTAVFFICMILITSLGRRKKAALLTSGFRPSVQ 240  
CC DB 181 TGSINSYCEKFFLPKMTITWPTAVFFICMILITSLGRRKKAALLTSGFRPSVQ 240  
CC  
CC QY 241 AHIKALLALSPFMLFISYFLSVFSAAGIFPPLDFKFWWSVITYCAAVHPITLLFSN 300  
CC DB 241 AHIKALLALSPFMLFISYFLSVFSAAGIFPPLDFKFWWSVITYCAAVHPITLLFSN 300  
CC  
CC QY 301 CRRLAVLKSRRSSRCGTP 318  
CC DB 301 CRRLAVLKSRRSSRCGTP 318  
CC  
CC RESULT 2  
CC Q646AS PRELIMINARY; PRT; 318 AA.  
CC ID 0646AS;  
CC DT 25-OCT-2004 (Tremblrel. 28, Created)  
CC DT 25-OCT-2004 (Tremblrel. 28, Last sequence update)  
CC DT 25-OCT-2004 (Tremblrel. 28, Last annotation update)

DE Taste receptor T2R56.  
OS Pan troglodytes (Chimpanzee).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.  
OX NCBI\_TaxID=9598;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Anne F., Yoav G., Orna M., Svante P.;  
RT "Evolution of bitter taste receptors in human and apes."  
RL Submitted (Aug-2004) to the EMBL/Genbank/DBD databases.  
DR EMBL; AY724901; AAU21114.1; -;  
KW Receptor.  
SQ SEQUENCE 318 AA; 36411 MW; 3DBB9FAC7A8A330 CRC64;  
CC  
CC Query Match 97.6%; Score 1638; DB 2; Length 318;  
CC Best Local Similarity 97.5%; Pred. No. 3.7e-113;  
CC Matches 310; Conservative 4; Mismatches 4; Indels 0; Gaps 0;  
CC  
CC QY 1 MNGDHWLVGSSVTDKKAIIIVTILLRLVAIAGNGFTTAAIGVWVLRMLPCDKLIV 60  
CC DB 1 MNGDHWLVGSSVTDKKAIIIVTILLRLVAIAGNGFTTAAIGVWVLRMLPCDKLIV 60  
CC  
CC QY 61 SLGASRFCLQSVVMGKTIYVFLHPMAFPYNPVLOFLAFQWDFLNAATLWSSTWLSVFCV 120  
CC DB 61 SLGASRFCLQSVVMGKTIYVFLHPMAFPYNPVLOFLAFQWDFLNAATLWSSTWLSVFCV 120  
CC  
CC QY 121 KIATFTHPVFPMVKHKLKSGMLPWWLFFSVGLSFTTILFFIGNHMYQNYLRNHLQPMNV 180  
CC DB 121 KIATFTHPVFPMVKHKLKSGMLPWWLFFSVGLSFTTILFFIGNHMYQNYLRNHLQPMNV 180  
CC  
CC QY 181 TGSINSYCEKFFLPKMTITWPTAVFFICMILITSLGRRKKAALLTSGFRPSVQ 240  
CC DB 181 TGSINSYCEKFFLPKMTITWPTAVFFICMILITSLGRRKKAALLTSGFRPSVQ 240  
CC  
CC QY 241 AHIKALLALSPFMLFISYFLSVFSAAGIFPPLDFKFWWSVITYCAAVHPITLLFSN 300  
CC DB 241 AHIKALLALSPFMLFISYFLSVFSAAGIFPPLDFKFWWSVITYCAAVHPITLLFSN 300  
CC  
CC QY 301 CRRLAVLKSRRSSRCGTP 318  
CC DB 301 CRRLAVLKSRRSSRCGTP 318  
CC  
CC RESULT 3  
CC Q646D0 PRELIMINARY; PRT; 318 AA.  
CC ID 0646D0;  
CC DT 25-OCT-2004 (Tremblrel. 28, Created)  
CC DT 25-OCT-2004 (Tremblrel. 28, Last sequence update)  
CC DT 25-OCT-2004 (Tremblrel. 28, Last annotation update)  
CC DE Taste receptor T2R56.  
CC OS Pan paniscus (Pygmy chimpanzee) (Bonobo).  
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.  
OX NCBI\_TaxID=9597;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Anne F., Yoav G., Orna M., Svante P.;  
RT "Evolution of bitter taste receptors in human and apes."  
RL Submitted (Aug-2004) to the EMBL/Genbank/DBD databases.  
DR EMBL; AY724866; AAU21089.1; -;  
KW Receptor.  
SQ SEQUENCE 318 AA; 36438 MW; 2658D7CDEB80C4C1 CRC64;  
CC  
CC Query Match 97.1%; Score 1630; DB 2; Length 318;  
CC Best Local Similarity 97.2%; Pred. No. 1.5e-112;  
CC Matches 309; Conservative 4; Mismatches 5; Indels 0; Gaps 0;  
CC  
CC QY 1 MNGDHWLVGSSVTDKKAIIIVTILLRLVAIAGNGFTTAAIGVWVLRMLPCDKLIV 60  
CC DB 1 MNGDHWLVGSSVTDKKAIIIVTILLRLVAIAGNGFTTAAIGVWVLRMLPCDKLIV 60  
CC  
CC QY 61 SLGASRFCLQSVVMGKTIYVFLHPMAFPYNPVLOFLAFQWDFLNAATLWSSTWLSVFCV 120



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Db      61 SLGASHRCLOSVMGKTIYVFLYPMAPXVNPVLOFLAFQMDPLNAATLMSWTLSVYCV 120
      121 KIATFTHPVFWMLKHKLSGMLPWWLFSSVGLSSTFTLLFFIGNHRMYQNTLRHLOPMNV 180
      121 KIATFTHPVFWMLKHKLSGMLPWWLFSSVGLSSTFTLLFFIGNHRMYQNTLRHLOPMNV 180
      181 TGDHSIRSYCEKFFYLPKMTITWPTAVFICMILLITSLGRHKKALLTTSGRFSPSVQ 240
      181 TGDHSIRSYCEKFFYLPKMTITWPTAVFICMILLITSLGRHKKALLTTSGRFSPSVQ 240
      241 AHKALALALISFAMLFISYFLSLVFSAGIFPPDLDFKFWMESVYILCAAVHPITLLFSN 300
      241 AHKALALALISFAMLFISYFLSLVFSAGIFPPDLDFKFWMESVYILCAAVHPITLLFSN 300
      301 CRLLRAVLKSRSSRCGTP 318
      301 CRLLRAVLKSRSSRCGTP 318

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## RESULT 4

064520 PRELIMINARY; PRT; 318 AA.

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AC      064520;
DT      25-OCT-2004 (TReMBLrel. 28, Created)
DT      25-OCT-2004 (TReMBLrel. 28, Last sequence update)
DT      25-OCT-2004 (TReMBLrel. 28, Last annotation update)
DE      Taste receptor T2R56.
OS      Gorilla gorilla (gorilla).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Gorilla.
OX      NCBI_TaxID=9593;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Anne F., Yoav G., Orna M., Svante P.;
RT      "Evolution of bitter taste receptors in human and apes.";
RL      Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
DR      EMBL; AY724923; AAU21129.1; -.
KW      Receptor.
SQ      SEQUENCE 318 AA; 36275 MW; 57DF5AC0369F48E7 CRC64;

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Query Match  
Best Local Similarity 96.7%; Score 1622; DB 2; Length 318;  
Matches 307; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

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QY      1 MNGDHMYLGSSVTDKKAIIIVTILLRLVAIAGNGFTTAAAGVWLRMLPCDKLLV 60
      1 MNGDHMYLGSSVTDKKAIIIVTILLRLVAIAGNGFTTAAAGVWLRMLPCDKLLV 60
      61 SLGASHRCLOSVMGKTIYVFLHMAPFPYNPVLOFLAFQMDPLNAATLMSWTLSVYCV 120
      61 SLGASHRCLOSVMGKTIYVFLHMAPFPYNPVLOFLAFQMDPLNAATLMSWTLSVYCV 120
      121 KIATFTHPVFWMLKHKLSGMLPWWLFSSVGLSSTFTLLFFIGNHRMYQNTLRHLOPMNV 180
      121 KIATFTHPVFWMLKHKLSGMLPWWLFSSVGLSSTFTLLFFIGNHRMYQNTLRHLOPMNV 180
      121 KIATFTHPVFWMLKHKLSGMLPWWLFSSVGLSSTFTLLFFIGNHRMYQNTLRHLOPMNV 180
      181 TGDHSIRSYCEKFFYLPKMTITWPTAVFICMILLITSLGRHKKALLTTSGRFSPSVQ 240
      181 TGDHSIRSYCEKFFYLPKMTITWPTAVFICMILLITSLGRHKKALLTTSGRFSPSVQ 240
      181 TGDHSIRSYCEKFFYLPKMTITWPTAVFICMILLITSLGRHKKALLTTSGRFSPSVQ 240
      181 TGDHSIRSYCEKFFYLPKMTITWPTAVFICMILLITSLGRHKKALLTTSGRFSPSVQ 240
      241 AHKALALALISFAMLFISYFLSLVFSAGIFPPDLDFKFWMESVYILCAAVHPITLLFSN 300
      241 AHKALALALISFAMLFISYFLSLVFSAGIFPPDLDFKFWMESVYILCAAVHPITLLFSN 300
      301 CRLLRAVLKSRSSRCGTP 318
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RESULT 5  
064507 PRELIMINARY; PRT; 318 AA.

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AC      064507;
DT      25-OCT-2004 (TReMBLrel. 28, Created)
DT      25-OCT-2004 (TReMBLrel. 28, Last sequence update)
DT      25-OCT-2004 (TReMBLrel. 28, Last annotation update)
DE      Taste receptor T2R56.
OS      Pongo pygmaeus (Orangutan).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Pongo.
OX      NCBI_TaxID=9600;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Anne F., Yoav G., Orna M., Svante P.;
RT      "Evolution of bitter taste receptors in human and apes.";
RL      Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
DR      EMBL; AY724986; AAU21172.1; -.
KW      Receptor.
SQ      SEQUENCE 318 AA; 36554 MW; D0F6A7F44C3FB5FA CRC64;

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Query Match  
Best Local Similarity 90.2%; Score 1514; DB 2; Length 318;  
Matches 289; Conservative 12; Mismatches 17; Indels 0; Gaps 0;

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QY      1 MNGDHMYLGSSVTDKKAIIIVTILLRLVAIAGNGFTTAAAGVWLRMLPCDKLLV 60
      1 MNGDHMYLGSSVTDKKAIIIVTILLRLVAIAGNGFTTAAAGVWLRMLPCDKLLV 60
      61 SLGASHRCLOSVMGKTIYVFLHMAPFPYNPVLOFLAFQMDPLNAATLMSWTLSVYCV 120
      61 SLGASHRCLOSVMGKTIYVFLHMAPFPYNPVLOFLAFQMDPLNAATLMSWTLSVYCV 120
      121 KIATFTHPVFWMLKHKLSGMLPWWLFSSVGLSSTFTLLFFIGNHRMYQNTLRHLOPMNV 180
      121 KIATFTHPVFWMLKHKLSGMLPWWLFSSVGLSSTFTLLFFIGNHRMYQNTLRHLOPMNV 180
      121 KIATFTHPVFWMLKHKLSGMLPWWLFSSVGLSSTFTLLFFIGNHRMYQNTLRHLOPMNV 180
      181 TGDHSIRSYCEKFFYLPKMTITWPTAVFICMILLITSLGRHKKALLTTSGRFSPSVQ 240
      181 TGDHSIRSYCEKFFYLPKMTITWPTAVFICMILLITSLGRHKKALLTTSGRFSPSVQ 240
      181 TGDHSIRSYCEKFFYLPKMTITWPTAVFICMILLITSLGRHKKALLTTSGRFSPSVQ 240
      181 TGDHSIRSYCEKFFYLPKMTITWPTAVFICMILLITSLGRHKKALLTTSGRFSPSVQ 240
      241 AHKALALALISFAMLFISYFLSLVFSAGIFPPDLDFKFWMESVYILCAAVHPITLLFSN 300
      241 AHKALALALISFAMLFISYFLSLVFSAGIFPPDLDFKFWMESVYILCAAVHPITLLFSN 300
      301 CRLLRAVLKSRSSRCGTP 318
      301 CRLLRAVLKSRSSRCGTP 318

```

## RESULT 6

064552 PRELIMINARY; PRT; 318 AA.

```

AC      064552;
DT      25-OCT-2004 (TReMBLrel. 28, Created)
DT      25-OCT-2004 (TReMBLrel. 28, Last sequence update)
DT      25-OCT-2004 (TReMBLrel. 28, Last annotation update)
DE      Taste receptor T2R56.
OS      Macaca mulatta (Rhesus macaque).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC      Cercopithecoidea; Macaca.
OX      NCBI_TaxID=9544;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Anne F., Yoav G., Orna M., Svante P.;
RT      "Evolution of bitter taste receptors in human and apes.";
RL      Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
DR      EMBL; AY725022; AAU21197.1; -.
KW      Receptor.
SQ      SEQUENCE 318 AA; 36278 MW; 15C342163F8F387B CRC64;

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Query Match  
Best Local Similarity 88.2%; Score 1480; DB 2; Length 318;  
Matches 285; Conservative 10; Mismatches 23; Indels 0; Gaps 0;

```

QY 1 MNGDHWLVSSVTDKAAIIVTLLRLVAIAGNGFTIATGVEVTLARMLLPCDKLIV 60
DB 1 MNGDHWLVSSVTDKAAIIVTLLRLVAIAGNGFTIATGVEVTLARMLLPCDKLIV 60
QY 61 SLGASRFCLQSVYMGKTIYVFLHPMAFPYVPVLOFLAFOQDFLNAATLMSVYFCV 120
DB 61 SLGASRFCLQSVYMGKTIYVFLHPMAFPYVPVLOFLAFOQDFLNAATLMSVYFCV 120
QY 121 KIATFHPVFWLKHLSGWLPMWLFFSVGLSFTTILFFIGNHRMYQNYLRNHLQPMNV 180
DB 121 KIATFHPVFWLKHLSGWLPMWLFFSVGLSFTTILFFIGNHRMYQNYLRNHLQPMNV 180
QY 181 TGDSTSYCEKFFLFPVKMTTMTPTAVFFICMILLITSLGRRKALLTTSGFREPSVQ 240
DB 181 TGDSTSYCEKFFLFPVKMTTMTPTAVFFICMILLITSLGRRKALLTTSGFREPSVQ 240
QY 241 AHFKALLALSPMLFISYFLSVFSAAGIFPPLDFKFWWESVIVLCAVHPILLFNSN 300
DB 241 AHFKALLALSPMLFISYFLSVFSAAGIFPPLDFKFWWESVIVLCAVHPILLFNSN 300
QY 301 CRIRAVLKSRSSRCGTP 318
DB 301 CRIRAVLKSRSSRCGTP 318
QY 301 RRLRAVLIERCRSSRCRTP 318
DB 301 RRLRAVLIERCRSSRCRTP 318

RESULT 7
TR35 MOUSE STANDARD; PRT; 312 AA.
ID 1 TR35 MOUSE STANDARD; PRT; 312 AA.
AC 07T09; 07M705;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Putative taste receptor type 2 member 35 (T2R35) (mT2R38).
GN Name=T2R35; Synonym=T2R38;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCB1_TaxID=10090;
RN 11 NCB1_TaxID=10090;
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RX MEDLINE=22709097; PubMed=12734386;
RA Conte C., Ebelling M., Marcuz A., Neff P., Andres-Barguin P.J.;
RT "Evolutionary relationships of the T2R3 receptor gene families in mouse and human.";
RL Physiol. Genomics 14:73-82(2003).
RN 121 TGDSTSYCEKFFLFPVKMTTMTPTAVFFICMILLITSLGRRKALLTTSGFREPSVQ 240
RP SEQUENCE FROM N.A.
RG The mouse genome sequencing consortium;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
RN 31 GENE STRUCTURE.
RX MEDLINE=22558047; PubMed=12679530; DOI=10.1093/molbev/mg083;
RA Shi P., Zhang Y., Yang H., Zhang Y.-P.;
RT "Adaptive diversification of bitter taste receptor genes in mammalian evolution.";
RL Mol. Biol. Evol. 20:805-814(2003).
CC -1- FUNCTION: Putative taste receptor which may play a role in the perception of bitterness.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -1- MISCELLANEOUS: Most taste cells may be activated by a limited number of bitter compounds; individual taste cells can discriminate among bitter stimuli.
CC -1- SIMILARITY: Belongs to the G-protein coupled receptor T2R family.
CC -1- CAUTION: Ref.1 sequence differs from that shown due to erroneous gene model prediction.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL collaboration - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial

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CC entities requires a license agreement (See http://www.itsb-sib.ch/announce/
CC or send an email to license@itsb-sib.ch).
CC -----
DR EMBL; AF532786; AAP4036.1; ALT SEQ.
DR EMBL; CA001174173; -. NOT ANNOTATED_CDS.
DR EMBL; BK001097; DAA01236.1; -.
DR GO; GO:0016021; C:integral to membrane; NAS.
DR GO; GO:0008527; F:taste receptor activity; NAS.
DR GO; GO:0001580; P:perception of bitter taste; sensory transdu. . .; NAS.
DR InterPro; IPR007960; T2R2_recept.
DR Pfam; PF05296; T2R2; 1.
KM G-protein coupled receptor; Receptor; Transmembrane.
FT DOMAIN 1 19 Extracellular (Potential).
FT TRANSMEM 20 40 1 (Potential).
FT DOMAIN 41 66 Cytoplasmic (Potential).
FT TRANSMEM 67 87 2 (Potential).
FT DOMAIN 88 97 Extracellular (Potential).
FT TRANSMEM 98 118 3 (Potential).
FT DOMAIN 119 140 Cytoplasmic (Potential).
FT TRANSMEM 141 161 4 (Potential).
FT DOMAIN 162 198 Extracellular (Potential).
FT TRANSMEM 199 219 5 (Potential).
FT DOMAIN 220 244 Cytoplasmic (Potential).
FT TRANSMEM 245 265 6 (Potential).
FT DOMAIN 266 277 Extracellular (Potential).
FT TRANSMEM 278 298 7 (Potential).
FT DOMAIN 299 312 Cytoplasmic (Potential).
FT CARBOHYD 179 179 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 312 AA; 35591 MW; 2B3811522589FC65 CRC64;

Query Match 57.2%; Score 960; DB 1; Length 312;
Best Local Similarity 58.8%; Pred. No. 4, 2e-63;
Matches 181; Conservative 46; Mismatches 81; Indels 0; Gaps 0;

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DB 1 MNGDHWLVSSVTDKAAIIVTLLRLVAIAGNGFTIATGVEVTLARMLLPCDKLIV 60
QY 61 SLGASRFCLQSVYMGKTIYVFLHPMAFPYVPVLOFLAFOQDFLNAATLMSVYFCV 120
DB 61 SLGASRFCLQSVYMGKTIYVFLHPMAFPYVPVLOFLAFOQDFLNAATLMSVYFCV 120
QY 121 KIATFHPVFWLKHLSGWLPMWLFFSVGLSFTTILFFIGNHRMYQNYLRNHLQPMNV 180
DB 121 KIATFHPVFWLKHLSGWLPMWLFFSVGLSFTTILFFIGNHRMYQNYLRNHLQPMNV 180
QY 181 TGDSTSYCEKFFLFPVKMTTMTPTAVFFICMILLITSLGRRKALLTTSGFREPSVQ 240
DB 181 TGDSTSYCEKFFLFPVKMTTMTPTAVFFICMILLITSLGRRKALLTTSGFREPSVQ 240
QY 241 AHFKALLALSPMLFISYFLSVFSAAGIFPPLDFKFWWESVIVLCAVHPILLFNSN 300
DB 241 AHFKALLALSPMLFISYFLSVFSAAGIFPPLDFKFWWESVIVLCAVHPILLFNSN 300
QY 301 CRIRAVLK 308
DB 301 PVLRAVLIK 308

RESULT 8
Q6TES2 PRELIMINARY; PRT; 321 AA.
ID Q6TES2;
AC Q6TES2;
DT 25-OCT-2004 (TEMBLrel. 28, Created)
DT 25-OCT-2004 (TEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TEMBLrel. 28, Last annotation update)
DE Putative taste receptor T2R28.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCB1_TaxID=10116;
RN 11 SEQUENCE FROM N.A.

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: February 4, 2005, 18:46:03 : Search time 4917 Seconds  
(without alignments)  
3133.772 Million cell updates/sec

Title: US-10-628-464-2

Perfect score: 1678

Sequence: 1 MGDHMYLGSVTDKAIL.....SNCRLRAVLKRRSRRCGTP 318

Scoring table:

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Xgapop 10.0, Xgapext 0.5  
Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 4708233 segs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

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-DB=GenEmbl -QFMT=faetap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bite -START=1 -END=1 -MATRIX=blomum62 -TRANS=human40.cdi -LIST=45  
-LOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
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Database :

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2: gb\_hlg:\*  
3: gb\_in:\*  
4: gb\_om:\*  
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7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sts:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vi:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1678	100.0	954	6	BD171274 Novel G p
2	1678	100.0	954	6	BD185566 Novel G p
3	1678	100.0	957	6	CQ738424 Sequence
4	1678	100.0	957	6	CQ800046 Sequence

5	1678	100.0	957	9	AY114094
6	1678	100.0	957	9	AY724955
7	1678	100.0	72045	9	AC092214
8	1638	97.6	957	9	AY724901
9	1630	97.1	957	9	AY724866
10	1622	96.7	957	9	AY724923
11	1514	95.7	957	9	AY724986
12	1480	88.2	957	9	AY725022
13	960	57.2	966	10	AF532786
14	960	57.2	203639	2	AC117625
15	953	56.8	966	10	AY62748
16	953	56.8	218921	2	AC097912
17	609	36.3	924	6	BD144615
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19	609	36.3	924	9	AY114093
20	609	36.3	1324	6	AX647249
21	609	36.3	175228	2	AC143343
22	609	36.3	200123	9	AC073264
23	608	36.2	921	6	CQ800004
24	608	36.2	924	9	AF494232
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26	607	36.2	924	9	AY724891
27	600.5	35.8	3437	6	AX097850
28	600	35.8	924	9	AY724869
29	596	35.5	924	9	AY724933
30	593.5	35.4	1295	6	AX097794
31	593.5	35.4	223179	2	AC128080
32	589.5	35.1	927	10	AF240768
33	580	34.6	924	9	AY724987
34	560	33.4	924	9	AY724831
35	560	33.4	924	9	AY725013
36	461	27.5	131565	2	AC143122
37	431	25.7	876	9	AY724993
38	427.5	25.5	186051	2	EX005324
39	427.5	25.5	200574	10	BX005304
40	427	25.4	8857	10	AF532785
41	425	25.3	885	10	AF532747
42	423	25.2	876	9	AY724890
43	422	25.1	876	9	AY724929
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#### ALIGNMENTS

RESULT 1	BD171274	954 bp	DNA	linear	PAT 17-JAN-2003
LOCUS	BD171274				
DEFINITION	Novel G protein-coupled receptor protein and DNA thereof.				
ACCESSION	BD171274.1	GI:27877086			
VERSION	BD171274.1	GI:27877086			
KEYWORDS	WO 02057309-A/1.				
SOURCE	WO 02057309-A/1.				
ORGANISM	Homo sapiens (human)				
REFERENCE	1 (bases 1 to 954)				
AUTHORS	Milwa, M., Ito, T., Shintani, Y. and Miyajima, N.				
TITLE	Novel G protein-coupled receptor protein and DNA thereof				
JOURNAL	Patent: WO 02057309-A 1 25-JUL-2002; TAKEDA CHEMICAL INDUSTRIES LTD, MASANORI MIWA, TAKASHI ITO, YASUSHI SHINTANI, NOBUYUKI MIYAJIMA				
COMMENT	OS Homo sapiens (human) PN WO 02057309-A/1 PD 25-JUL-2002 PF 17-JAN-2002 WO 2002JP000271 PR 18-JAN-2001 JP 01P 010814, 30-MAR-2001 JP 01P 102558 PI MASANORI MIWA, TAKASHI ITO, YASUSHI SHINTANI, NOBUYUKI MIYAJIMA PC CQ7K16/78, CQ7K16/28, PC C12P21/02, C12P21/08, C12Q1/02, C12Q1/68, G01N33/15, G01N33/53, PC G01N33/566,				

AL1K38/00, A61K45/00, A61P1/00, A61P3/00, A61P5/00, A61P9/00, A61P11/00,  
PC A61P25/28, A61P35/00, A61P37/00  
CC Novel G protein-coupled receptor protein and DNA thereof FH  
Key Location/Qualifiers  
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/db\_xref="taxon:9606"

ORIGIN

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US-10-628-464-2 (1-318) x BD171274 (1-954)

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DB 121 GCCTGGCGCTGAGTGGGTGCTACGAGATGTGTGCTTGTATAGTATTGCTT 180  
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QY 101 AspPheLeuAaAaIaThIleuTrpSeSeThITrPLeuSeVaLPhyTyCyVa 120  
DB 301 GACTTCTGAATGCTGCACCTTATGTCTCTACCTGCTCAGTGTCTTCTTATGTG 360  
QY 121 LysIleAaThIePhThIaProVaLPhaPheTrIleuLysHieLysLeuSeGIyTP 140  
DB 361 AAATATGCTACTTACCCACCTGCTCTTCTGCTTAAGCAACAAGTTGCTGGGTTG 420  
QY 141 LeuProTrpMetLeuPheSeSeSeVaLGIyLeuSeSePhThIleuPhePhe 160  
DB 421 CTACCAAGATGCTCTTCACTGTAAGGCTCTCCAGCTTCAACACCATTTATTTTTC 480  
QY 161 IleGIyAaHieSaRyMeTyGIaAeTyLeuAaGyAaHieSeuGIInProTPAaVa 180  
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QY 181 ThrGIyAaSeRieIleAaSeTyTyCyGIyLysPheTyTrPLeuProLeuLysMeIle 200  
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RESULT 2  
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LOCUS BD185566 954 bp DNA linear PAT 17-JUN-2003  
DEFINITION Novel G protein-coupled receptor and its DNA.  
ACCESSION BD185566  
VERSION BD185566.1 GI:31877766  
KEYWORDS JP 2002360279-A/1.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
REFERENCE  
AUTHORS Miwa,M., Ito,T., Shintani,Y. and Miyajima,N.  
TITLE Novel G protein-coupled receptor and its DNA  
JOURNAL Patent: JP 2002360279-A I 17-DEC-2002;  
TAKEDA CHEMICAL INDUSTRIES LTD  
OS Homo sapiens (human)  
PN JP 2002360279-A/1  
PD 17-DEC-2002  
PF 17-JAN-2002 JP 2002008445  
PI MASANORI MIWA, TAKASHI ITO, YASUSHI SHINTANI, NOBUYUKI MIYAJIMA  
PC C12N15/09, A61K39/395, A61K39/395, A61K45/00, A61P1/00, A61P3/00,  
PC A61P9/00, A61P11/00, A61P25/28, A61P29/00, A61P31/00, A61P35/00, PC  
A61P37/00,  
PC C07K14/705, C07K16/28, C12N1/15, C12N1/19, C12N1/21, C12N5/10, PC  
C12P21/02, C12Q1/02, C12Q1/68, G01N33/15, G01N33/50, G01N33/53, G01N33/53, PC  
G01N33/566,  
PC C12N15/00, C12N5/00  
CC Novel G protein-coupled receptor and its DNA  
FH Key Location/Qualifiers  
FT source 1..954  
Location/Qualifiers  
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/organism="Homo sapiens"  
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ORIGIN

Alignment Scores:

Pred. No.:	5,39e-142	Length:	954
Score:	1678.00	Matches:	318
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	6	Gaps:	0

US-10-628-464-2 (1-318) x BD185566 (1-954)

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QY 21 ValThIleuLeuLeuLeuAaGlyVaLaIleIleAaIySaNGIyPhelIeThRa 40  
DB 61 GTTACCAATTTTACTCTTTTACCGCTGGTGAATAGCAGGACGATGGCTTCATCAGCTG 120

QY 41 AlaLeuGlyValGluTrpValLeuArgArgMetLeuProCysAspLysLeuVal 60  
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DB 181 AGCTTAGGGGCGCTCTGCTTCTGTCTGACGACATGGTAATGGTAAGACATTATGTT 240  
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DB 241 TTCTTGATCCGATGGGCTTCCCATACACCTGTACTGAGTTCTAGCTTTCAGTGG 300  
QY 101 AspPheLeuAsnAlaAlaThrLeuTyrSerSerThrTrpLeuSerValPheTyrCysVal 120  
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QY 121 LysIleAlaThrPheThrHisProValPhePheTrpLeuLysHisLysLeuSerGlyTrp 140  
DB 361 AAATTTGCTACCTTACCCACCCCTGTCTTCTGGCTAAAGCACAAGTTGTGGGTGG 420  
QY 141 LeuProTrpMetLeuPheSerSerValGlyLeuSerSerPheThrTrpIleLeuPhePhe 160  
DB 421 CTACCATGATGCTCTTCAAGCTGTAGGGCTCTCCAGCTTCCACACCATTTCTATTGTT 480  
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DB 541 ACTGGCATATGCAATACGAGAGTACTGAGAAATTCATCTCTTCCCTTAAATAATGATT 600  
QY 201 ThrTrpThrMetProThrAlaValPhePheIleCysMetIleLeuLeuIleThrSerLeu 220  
DB 601 ACTTGAGCAATGCCACCTGCTGTCTTTTTCATTGTCATGATTTGCTCATCATCTCTG 660  
QY 221 GlyArgHisArgLysLysValAlaLeuLeuThrThrSerGlyPheArgGlnProSerValGln 240  
DB 661 GGAAGACACAGAAAGAGGCTCTCTTAACAACCTCAGATTCAGAGGCCAGGTGTCAG 720  
QY 241 AlaHisIleLysAlaLeuLeuAlaLeuLeuSerPheAlaMetLeuPheIleSerTyrPhe 260  
DB 721 GCACACATTAAGGCTGTGCTGCTCTCTCTCTTTTGCATNGCTCTTCACTCATCATTTTC 780  
QY 261 LeuSerLeuValPheSerAlaAlaGlyIlePheProProLeuAspPheLysPheTrpVal 280  
DB 781 CTGTCACTGGTGTTCAGTGTGTCAGAGTATTTTTCACCTCTGAGCTTTAAATTCGGGTG 840  
QY 281 TrpGlnSerValIleTyrTrpLeuCysAlaAlaValHisProIleIleLeuLeuPheSerAsn 300  
DB 841 TGGAGTCACTGATTTATCTGTGTGAGCAGCATTAACCCATCATTTGCTTTAGCAAC 900  
QY 301 CysArgLeuArgAlaValAlaLeuLysSerArgArgSerSerArgCysGlyThrPro 318  
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RESULT 3  
CQ738424 957 bp DNA linear PAT 03-FEB-2004  
LOCUS CQ738424  
DEFINITION Sequence 24358 from Patent WO02068579.  
ACCESSION CQ738424  
VERSION CQ738424.1 GI:42339256  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
AUTHORS Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.  
TITLE Kites, such as nucleic acid arrays, comprising a majority of  
humanexons or transcripts, for detecting expression and other uses  
thereof

JOURNAL Patent: WO 02068579-A 24358 06-SEP-2002;  
PE Corporation (NY) (US)  
FEATURES Location/Qualifiers  
source 1..957  
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ORIGIN

Alignment Scores:  
Pred. No.: 5,41e-142 Length: 957  
Score: 1678.00 Matches: 318  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: Gaps: 0

US-10-628-464-2 (1-318) x CQ738424 (1-957)

QY 1 MetAsnGlyValAspHisMetValLeuGlySerSerValThrAspLysValAlaIleLeu 20  
DB 1 ATGAATGAGACACCAATGTTCTTAGATCTTCGGTACTGACAGAAAGGCATCATCTTG 60  
QY 21 ValThrIleLeuLeuLeuArgLeuValAlaIleAlaGlyAsnGlyPheIleThrAla 40  
DB 61 GTTACCATTTTACTCTCTTTTACGCTGTGATGCAATGACAGGCAATGGCTTCATCTGCT 120  
QY 41 AlaLeuGlyValGluTrpValLeuArgArgMetLeuProCysAspLysLeuVal 60  
DB 121 GCTCTGGGCGGTGGAGTGGGTCTACGAGAAATGTTGTGCTTGTGATTAATGTTGTT 180  
QY 61 SerLeuGlyValAspArgPheCysLeuGlnSerValAlaMetGlyLysThrIleTyrVal 80  
DB 181 AGCTTAGGGGCGCTCTGCTTCTGTCTGACGTAGTGAATGGTAAGCAATTAATGTT 240  
QY 81 PheLeuHisProMetAlaPheProTyrAsnProValLeuGlnPheLeuAlaPheGlnTrp 100  
DB 241 TTCTTGATCCGATGGGCTTCCCATACACCTGTACTGAGTTCTAGCTTTCAGTGG 300  
QY 101 AspPheLeuAsnAlaAlaThrLeuTyrSerSerThrTrpLeuSerValPheTyrCysVal 120  
DB 301 GACTTCTGAATGCTGCACCTTAATGGTCCCTTCACTGAGTGTCTTCTATTTGTTG 360  
QY 121 LysIleAlaThrPheThrHisProValPhePheTrpLeuLysHisLysLeuSerGlyTrp 140  
DB 361 AAATTTGCTACCTTACCCACCCCTGTCTTCTGGCTAAAGCACAAGTTGTGGGTGG 420  
QY 141 LeuProTrpMetLeuPheSerSerValGlyLeuSerSerPheThrTrpIleLeuPhePhe 160  
DB 421 CTACCATGATGCTCTTCAAGCTGTAGGGCTCTCCAGCTTCCACACCATTTATTTTC 480  
QY 161 IleGlyAsnHisArgMetTyrGlnAsnTyrLeuArgAsnHisLysGlnProTrpAsnVal 180  
DB 481 ATAGGCAACCAACAAGATGATCAAGACTATTAAAGAACCACTTCAACCTTGAATGTC 540  
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QY 221 GlyArgHisArgLysLysValAlaLeuLeuThrThrSerGlyPheArgGlnProSerValGln 240  
DB 661 GGAAGACACAGAAAGAGGCTCTCTTCAACCTCAGATTCAGAGGCCAGGTGTCAG 720  
QY 241 AlaHisIleLysAlaLeuLeuAlaLeuLeuSerPheAlaMetLeuPheIleSerTyrPhe 260  
DB 721 GCACACATTAAGGCTGTGCTGCTCTCTCTTTTGCATNGCTCTTCACTCATCATTTTC 780  
QY 261 LeuSerLeuValPheSerAlaAlaGlyIlePheProProLeuAspPheLysPheTrpVal 280

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Db      781 CTGTCACTGGTGTTCAGTGTGTCGAGGATTTTCCACCTTGAGCTTTAAATTCGTGGGTG 840
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Db      841 TGGAGTCACTGATTTATCTGTGTGTGCGAGCTTCACTTCTGCTTCTTCAAGCAG 900
Qy      301 CysArgLeuAlaValLeuLeuYsSerArgSerSerArgCysGlyThrPro 318
Db      901 TGCAGGCTGAGAGCTGTGTGTAAGAGTCCGCTTCTCAAGGTGTGGAGCACTT 954

RESULT 4
LOCUS   CQ800046                      957 bp    DNA          linear    PAT 28-APR-2004
DEFINITION
Sequence 50 from Patent WO2004029087.
CQ800046
VERSION  CQ800046.1  GI:46848968
KEYWORDS
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
           Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
1 Bufo, B., Hofmann, T., Krautwurst, D., Kuhn, C. and Meyerhof, W.
  Bitter taste receptors
  Patent: WO/2004029087-A 50 08-APR-2004;
  DEUTSCHES INSTITUT FUER ERNAHRUNGSGESUNDHUNG (DE)

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ORIGIN

Alignment Scores:
Pred. No.:      5 11e-142      Length:      957
Score:          1678.00      Matches:      318
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:    100.00%      Indels:      0
DB:             6              Gaps:      0

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Qy      61 SerLeuGlyAlaSerArgPheCysLeuGlnSerValValMetGlyYsThrIleYrVal 80
Db      181 AGCTTAGGGGCTCTGCTCTGTCTGCTGACATGAGTGTATGGGTAAAGACATTTATGTT 240
Qy      81 PheLeuHisProMetCAlaPheProTyrAsnProValLeuGlnPheLeuAlaPheGlnTTP 100
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Qy      101 AspPheLeuAsnAlaAlaThrLeuTTPSerSerThrTTPLeuSerValPheTyrCysVal 120
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Qy      121 LysIleAlaThrPheThrHisProValPhePheTTPLeuYsHisYsLeuSerGlyTTP 140
Db      361 AAAATTGCTACCTTCAACCAACCGCTGCTTCTTCTGCTTAAGCACAAGATTGTCTGGGTG 420
Qy      141 LeuProTTPMetLeuPheSerSerValGlyLeuSerSerPheThrThrIleLeuPhePhe 160

Db      421 CTACCATGAGTCTCTTCAGCTCTGTAGGGCTCTCCAGCTTCACCACTTATTTTTC 480
Qy      161 IleGlyAsnHisArgMetTyrGlnIleThrYrLeuArgAsnHisLeuGlnProTTPAsnVal 180
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Qy      221 GlyArgHisArgYsYsAlaLeuLeuThrThrThrSerGlyPheArgGlnProSerValGln 240
Db      661 GGAGACACACAGAAAGAGGCTCTCTTACACCTTCAGATTCGAGAGCCAGTGTGGAG 720
Qy      241 AlaHisIleYsAlaLeuLeuAlaLeuLeuSerPheAlaMetLeuPheIleSerTyrPhe 260
Db      721 GCACACATAAAGGCTGTGCTGGCTGCTCTCTCTTTGGCCATGCTCTTCATTCATATTTC 780
Qy      261 LeuSerLeuValPheSerAlaAlaGlyIlePheProProLeuAspPheYsPheTTPVal 280
Db      781 CTGTCACTGGTGTTCAGTGTCTGAGGATATTTTCCACCTTGACTTTAAATTCGGGTG 840
Qy      281 TTPGLUserVal1IetYrleuCysAlaAlaValHisProIleIleLeuLeuPheSerAsn 300
Db      841 TGGAGTCACTGATTTATCTGTGTGTGCGAGCTTCACTTCACTTATCTGCTTTCAGCAG 900
Qy      301 CysArgLeuAlaValLeuLeuYsSerArgSerSerArgCysGlyThrPro 318
Db      901 TGCAGGCTGAGAGCTGTGTGTAAGAGTCCGCTTCTCAAGGTGTGGAGCACTT 954

RESULT 5
LOCUS   AY114094                      957 bp    DNA          linear    PRI 28-FEB-2003
DEFINITION
Homo sapiens putative taste receptor T2R60 gene, complete cde.
AY114094
VERSION  AY114094.1  GI:28603637
KEYWORDS
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
           Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
1 Conte, C., Ebeling, M., Marcuz, A., Nef, P. and Andres-Barquin, P.J.
  Identification and characterization of human taste receptor genes
  belonging to the TAS2R family
  Cytogenet. Genome Res. 98 (1), 45-53 (2002)

JOURNAL  MEDLINE
PUBMED   22471936
12584440

REFERENCE
2 (bases 1 to 957)
Conte, C., Ebeling, M., Marcuz, A., Nef, P. and Andres-Barquin, P.J.
Direct Submision
Submitted (17-MAY-2002) Pharma Research Basel, F. Hoffmann-La Roche
Ltd., Grenzacherstrasse 124, Basel CH-4070, Switzerland

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## ORIGIN

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## Alignment Scores:

Align. No.: 5,41e-142 Length: 957  
Score: 1678.00 Matches: 318  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: Gaps: 0

US-10-628-464-2 (1-318) x AY114094 (1-957)

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Qy 21 ValThrIleLeuLeuLeuLeuAArgLeuValAlaIleIleIleIleIleIleIleIleIle 40  
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Qy 41 AlaleuGlyValGluTrpValIleuAArgMetLeuLeuProCysAspIleLeuVal 60  
Db 121 GCTCTGGGCGGTGAGTGGGTCTACGAGAAATGTTGCTTGTGATTAAGTTATGGTT 180  
Qy 61 SerLeuGlyAlaSerAArgPheCysLeuGlnSerValValMetGlyIleTrpVal 80  
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Qy 301 CysAArgLeuAArgAlaValLeuLysSerAArgSerSerAArgCysGlyThrPro 318  
Db 901 TGCAGGCTGAGACGTGTGTAAGAGTGTGCTTCTTCAAGAGTGTGGACACCT 954

RESULT 6  
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LOCUS Homo sapiens chromosome 7 taste receptor T2R56 gene, complete cds.  
DEFINITION  
ACCESSION AY724955  
VERSION AY724955.1 GI:51989208  
KEYWORDS  
SOURCE  
ORGANISM Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
AUTHORS Anne,F., Yoav,G., Orna,M. and Svante,P.  
TITLE Evolution of bitter taste receptors in human and apes  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 957)  
AUTHORS Anne,F., Yoav,G., Orna,M. and Svante,P.  
TITLE Direct Submission  
JOURNAL Submitted (12-AUG-2004) Genetics, Max-Planck Institute for  
Evolutionary Anthropology, Deutscher Platz 6, Leipzig 04103,  
Germany

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## ORIGIN

Alignment Scores:  
Align. No.: 5,41e-142 Length: 957  
Score: 1678.00 Matches: 318  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: Gaps: 0

US-10-628-464-2 (1-318) x AY724955 (1-957)

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Db 1 ATGAATGGAGACCAATGGTCTTAGATCTTCGGTGAAGTGAAGAGGCCATCATCTTG 60  
Qy 21 ValThrIleLeuLeuLeuAArgLeuValAlaIleIleIleIleIleIleIleIleIle 40  
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Db	301	GACTTCCGAAATGCTGCCACACCTTAAGGTCCTTACCTGGCTCAGTGTCTTCAATGTTGTG	360
Oy	121	LysIleAlaTrpPheThrHisProValPhePheTrpLeuLysHisLysLeuSerClyTrp	140
Db	361	AAATATGCTTACCTTACCCACCCCTCTCTCTTCTGGCTTAAGACACAACTGTCTGGGTGG	420
Oy	141	LeuProTrpMetLeuPheSerSerValGlyLeuSerSerPheThrThrIleLeuPhePhe	160
Db	421	CTACCATGATGCTCTTCCAGCTCTGTAGGGCTCTCAGCTTCCACCACTTCTAATTTTTC	480
Oy	161	IleGlyAsnHisArgMetTyTrGlnAsnTyTrLeuArgAsnHisLeuGlnProTrpAsnVal	180
Db	481	ATAGGCAACCAACAGATGATTCAGAACTTAATTAAGAAACCAATCTCAACCTTGAATGTC	540
Oy	181	ThrGlyAspSerIleArgSerTyTrCysGlyLysPheTyTrLeuPheProLeuLysMetIle	200
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Oy	201	ThrTrpIleMetProThrAlaValPhePheIleCysMetIleLeuLeuIleThrSerLeu	220
Db	601	ACTTGACAAATGCCACCTGCTGTCTTTTTCATTGCAATGATTTTCTCATCATCTCTG	660
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DEFINITION	Homo sapiens	BAC clone RP11-811J9 from 7,	complete sequence.
ACCESSION	AC092214		
VERSION	AC092214.3	GI:16931065	
KEYWORDS	HTG.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens (human)		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	Hillier, L.M., Fulton, R.S., Fulton, L.A., Graves, T.A., Pepin, K.H., Wagner-McInerney, C., Layman, D., Maas, J., Jaeger, S., Walker, R., Wyllie, K., Sekhon, B., Becker, M.C., O'Laughlin, M.D., Schaller, M.E., Fewell, G.A., Delahunty, K.D., Minter, T.L., Nash, W.E., Cordes, M., Du, H., Sun, H., Edwards, J., Bradshaw-Cordum, H., Ali, J., Andrews, S., Isak, A., Vandbrunt, A., Nguyen, C., Du, F., Lamar, B., Courtney, L., Hakicki, J., Ozeraky, P., Bielicki, L., Scott, K., Holmes, A., Watkins, R., Harris, A., Strong, C.M., Hou, S., Tomlinson, C., Dauphin-Kohlberg, S., Kozlowski-Reilly, A., Leonard, S., Rohlfing, T., Rock, S.M., Tin-Wei, A.M., Abbott, A., Minx, P., Maupin, R., Stromwater, C., Latreille, P., Miller, N., Johnson, D., Murray, J., Woese, J.P., Wendt, M.C., Yang, S.P., Schultz, B.R., Wallis, J.W., Speth, J., Bieri, T.A., Nelson, J.O., Berkowicz, N., Woldmann, P.E., Cook, L.L., Hickenbotham, M.T., Eldred, J., Williams, D., Bedell, J.A.,		

TITLE	Journal of Molecular Evolution
JOURNAL	Journal of Molecular Evolution
MEDLINE	12853999
PUBMED	12853999
REFERENCE	2 (bases 1 to 72045)
AUTHORS	Doebber, A., Elliott, G., Kozlowski, A. and Sun, H.
TITLE	The sequence of Homo sapiens BAC clone RP11-811J9
JOURNAL	Unpublished (2001)
REFERENCE	3 (bases 1 to 72045)
AUTHORS	Waterston, R.H.
TITLE	Direct Submission
JOURNAL	Submitted (29-JUN-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
REFERENCE	4 (bases 1 to 72045)
AUTHORS	Waterston, R.H.
TITLE	Direct Submission
JOURNAL	Submitted (15-NOV-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
REFERENCE	5 (bases 1 to 72045)
AUTHORS	Waterston, R.H.
TITLE	Direct Submission
JOURNAL	Submitted (10-JUN-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
REFERENCE	6 (bases 1 to 72045)
AUTHORS	Waterston, R.
TITLE	Direct Submission
JOURNAL	Submitted (31-JUN-2004) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
REFERENCE	7 (bases 1 to 72045)
AUTHORS	Wilson, R.
TITLE	Direct Submission
JOURNAL	Submitted (31-JUN-2004) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
COMMENT	On Nov 15, 2001 this sequence version replaced g1:15625026.

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

**MAPPING INFORMATION:** The sequence of this clone was established as part of a mapping and sequencing collaboration between the NIGRI Chromosome 7 Mapping Project (Eric D. Green, Director), John D. McPherson in the Department of Genetics (Washington University), and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see





QY 161 ILEGLYASNHISARGMETYRGINAENTYRLEUARGASNHISLEUGINPROTPAENVAL 180  
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 QY 181 THGLYASPERILAEAGSERTYCYGGLULYPHEHYRLEUPHEPROLEULYMERILE 200  
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 QY 261 LEUSERLEUVALPHESERIALAALAGLYILEPHEPROLEUAPPHELYSPHETRPVAL 280  
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 QY 281 TRPGIUSERVALILETYRLEUCYSAALAAVALHISPROLLEILEULEUPHESERASN 300  
 DB 63657 TGGGAGTCAGTGAATTTATCTGTGTGACGACATTCACCCCATTCATCTGCTCTTCAGAAC 63716  
 QY 301 CYARGLEUARGALALEULEUSERARGSERSERARGCYSGLYTHRPRO 318  
 DB 63717 TGCAGGCTGAGAGCTGTGCTGAAGAGTGTGCTCTCAAGGTGTGGACACCT 63770  
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 LOCUS AY724901 957 bp DNA linear PRI 18-SEP-2004  
 DEFINITION Pan troglodytes chromosome 7 taste receptor T2R56 gene, complete  
 ACCESSION AY724901  
 VERSION AY724901.1 GI:51989117  
 KEYWORDS Pan troglodytes (chimpanzee)  
 SOURCE Pan troglodytes  
 ORGANISM Pan troglodytes  
 Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.  
 1 (bases 1 to 957)  
 Anne, F., Yoav, G., Orna, M. and Svante, P.  
 Evolution of bitter taste receptors in human and apes  
 Unpublished  
 2 (bases 1 to 957)  
 Anne, F., Yoav, G., Orna, M. and Svante, P.  
 Direct Submission  
 Submitted (12-AUG-2004) Genetica, Max-Planck Institute for  
 Evolutionary Anthropology, Deutscher Platz 6, Leipzig 04103,  
 Germany  
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Alignment Scores:  
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 Best Local Similarity: 97.48% Mismatches: 0  
 Query Match: 97.62% Indels: 0  
 DB: 9 Gaps: 0  
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 QY 21 VALTHRIILEULEULEUARGLEUVALAIALAGLYASGLYPHEILETHRALA 40  
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 DB 121 GCTGTGGCGTGAGAGTGGGTGCTACCGAGAAATGTTGCTGTGATTAAGTTATGTTT 180  
 QY 61 SERLEUGLYALASERARGPHECYSEUGINSERVALVAMEGLIYRTHRIETRYVAL 80  
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 DB 241 TTCTTGATCCGATGGCCTTCCATACMACCTGTACTGAGTTTCTAGCTTCCAGTGG 300  
 QY 101 ASPPHELEUASNALAATHRIEUTRPSERSETHTRIPLEUSERVALPHERYCYVAL 120  
 DB 301 GACTTCCTGAATCTGCCACCTTATGATGTTCTTACCTGGCTCAGTGTCTTCTATGTTG 360  
 QY 121 LYSILALASRPHETHRHSRPROVALPHEPETHRLEULYHISLYSEUSERGYLTRP 140  
 DB 361 AAAATTGCTACCTTCAACCCACCTGTCTTCTTGTGCTAAAGCAAGTGTGTGGAGTGG 420  
 QY 141 LEUPROTPHMECPHEUSERSERVALGLYLEUSERSERPHEHTRHRIELEUPHEPHE 160  
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 QY 161 ILEGLYASNHISARGMETYRGINAENTYRLEUARGASNHISLEUGINPROTPAENVAL 180  
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 QY 281 TRPGIUSERVALILETYRLEUCYSAALAAVALHISPROLLEILEULEUPHESERASN 300  
 DB 841 TGGGAGTCAGTGAATTTATCTGTGTGACGACGATTCACCCCATCATCTGCTCTTCAGAAC 900  
 QY 301 CYARGLEUARGALALEULEUSERARGSERSERARGCYSGLYTHRPRO 318  
 DB 901 TGCAGGCTGAGAGCTGTGCTGAAGAGTGTGCTCTCAAGGTGTGGACACCT 954

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RESULT 9
AY724866      957 bp  DNA  linear  PRI 18-SEP-2004
LOCUS        Pan paniscus chromosome 7 taste receptor T2R56 gene, complete cds.
DEFINITION
ACCESSION   AY724866
VERSION     AY724866.1  GI:51989057
KEYWORDS
SOURCE      Pan paniscus (pygmy chimpanzee)
ORGANISM    Pan paniscus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Pan.
REFERENCE   1 (bases 1 to 957)
AUTHORS     Anne, F., Yoav, G., Orna, M. and Svante, P.
TITLE       Evolution of bitter taste receptors in human and apes
JOURNAL     Unpublished
2 (bases 1 to 957)
REFERENCE   Anne, F., Yoav, G., Orna, M. and Svante, P.
AUTHORS     Submitted (12-AUG-2004) Genetics, Max-Planck Institute for
TITLE       Evolutionary Anthropology, Deutscher Platz 6, Leipzig 04103,
JOURNAL     Germany

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Source      Location/Qualifiers
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ORIGIN
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Score:          1630.00      Matches:      309
Percent Similarity: 98.43%      Conservative: 4
Best Local Similarity: 97.17%      Mismatches: 5
Query Match:    97.14%      Indels:      0
DB:              Gaps:      0

US-10-628-464-2 (1-318) x AY724866 (1-957)

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Db      61 GTTACCAATTTTACCTCTTTTACGCTTAGTACATACAGCAATGAGCTTCATCATCTGCT 120
QY      41 AlaLeuGlyValGluTPValLeuArgArgMetLeuLeuProCysAspIlySlyLeuVal 60
Db      121 GCTCTGGCGGTGAGTGGCTCTACGAGAAATGTTGCTTGTGTAATTAATTGTT 180
QY      61 SerLeuGlyAlaSerArgPheCysLeuGlnSerValValMetGlyIlyThrIleTyrVal 80
Db      181 AGCCTAGGGGCTCTCTCACTTCTGCTGACGACATGATAGGTAAGACCATTTATGTT 240
QY      81 PheLeuHisProMetAlaPheProTyrAsnProValLeuGlnPheLeuAlaPheGlnTyr 100
Db      241 TTCTGTATCCGATGGAGCTTCTTCATACACCTTACTGACGATTCTTAGCTTCCAGTGG 300
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QY      201 ThrTyrPheCProThrAlaValPhePheIleCysMetIleLeuLeuIleThrSerLeu 220
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QY      261 LeuSerLeuValPheSerAlaIaIaGlyIlePheProProLeuAspPheLysPheTyrVal 280
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QY      301 CysArgLeuArgAlaValLeuLysSerArgArgSerSerArgGlyIlyThrPro 318
Db      901 TGCAGGCTGAGACCTGCTGTAAGAGTGGCTGTTCTTCCAGAGTGTGGACACCT 954

RESULT 10
AY724923      957 bp  DNA  linear  PRI 18-SEP-2004
LOCUS        Gorilla gorilla chromosome 7 taste receptor T2R56 gene, complete
DEFINITION
ACCESSION   AY724923
VERSION     AY724923.1  GI:51989154
KEYWORDS
SOURCE      Gorilla gorilla (gorilla)
ORGANISM    Gorilla gorilla
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Gorilla.
REFERENCE   1 (bases 1 to 957)
AUTHORS     Anne, F., Yoav, G., Orna, M. and Svante, P.
TITLE       Evolution of bitter taste receptors in human and apes
JOURNAL     Unpublished
2 (bases 1 to 957)
REFERENCE   Anne, F., Yoav, G., Orna, M. and Svante, P.
AUTHORS     Submitted (12-AUG-2004) Genetics, Max-Planck Institute for
TITLE       Evolutionary Anthropology, Deutscher Platz 6, Leipzig 04103,
JOURNAL     Germany

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pred. No.: 6.06e-137 Length: 957  
Score: 1622.00 Matches: 307  
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Best Local Similarity: 96.54% Mismatches: 7  
Query Match: 96.66% Indels: 0  
DB: Gaps: 0

US-10-628-464-2 (1-318) x AY724986 (1-957)

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QY 21 ValThrIleLeuLeuLeuLeuArgLeuValAlaIleAlaGlyAsnGlyPheIleIleThra 40  
DB 61 GTTACCATTTTACTCTCTTACCGCTGTAGCAATAGCAGCAATGGCTTCATCATGCT 120  
QY 41 AlaLeuGlyValAlaIleUtrPValLeuArgArgMetLeuLeuProCysAspLysLeuLeuVal 60  
DB 121 GCTCTGGCGGTGAGTGGGTGTACAGAGAAATGTGTGCTTGTGATGATGATGATG 180  
QY 61 SerLeuG1YAlaSerArgPheCysLeuGlySerValValMetGlyLysThrIleYVal 80  
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DB 781 CTGTCACTGATGTTCTGACTGCTGAGGTATTTTCCACTTGGACTTAAATCTGGGTG 840  
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DB 901 TGCAGGCTAGAGCTGTGCTGAGAAAGTTGCCGTCTCTCAAGGTGTGTGACACT 954

## RESULT 11

AY724986 957 bp DNA linear PRI 18-SEP-2004  
LOCUS Pongo pygmaeus chromosome 7 taste receptor T2R56 gene, complete  
DEFINITION cds  
VERSION AY724986  
KEYWORDS AY724986.1 GI:51989260

ORGANISM Pongo pygmaeus (orangutan)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pongo.

REFERENCE 1 (bases 1 to 957)  
AUTHORS Anne,F., Yoav,G., Orna,M. and Svante,P.  
JOURNAL Evolution of bitter taste receptors in human and apes  
TITLE Unpublished  
AUTHORS 2 (bases 1 to 957)  
TITLES Anne,F., Yoav,G., Orna,M. and Svante,P.  
JOURNAL Direct Submission  
AUTHORS Submitted (12-AUG-2004) Genetics, Max-Planck Institute for  
Evoluntionary Anthropology, Deutscher Platz 6, Leipzig 04103,  
Germany

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## ORIGIN

## ALIGNMENT SCORES:

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Percent Similarity: 94.65% Conservative: 12  
Best Local Similarity: 90.88% Mismatches: 17  
Query Match: 90.23% Indels: 0  
DB: Gaps: 0

US-10-628-464-2 (1-318) x AY724986 (1-957)

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DB 1 ATGAATGGAGACCAATGTTCTTAGATCTTCGGTACTGACAGAGAGCCATCATCTTG 60  
QY 21 ValThrIleLeuLeuLeuArgLeuValAlaIleAlaGlyAsnGlyPheIleIleThra 40  
DB 61 GTTACCATTTTACTCTCTTACCGCTGTAGCAATAGCAGCAATGGCTTCATCATGCT 120  
QY 41 AlaLeuGlyValAlaIleUtrPValLeuArgArgMetLeuLeuProCysAspLysLeuLeuVal 60  
DB 121 GCTCTGGCGGTGAGTGGGTGTACAGAGAAATGTGTGCTTGTGATGATGATGATG 180

Qy 61 SerLeuGlyValAspSerArgPheCysLeuGlnSerValValMetGlyLysThrIleTyrVal 80  
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 Db 301 GACTTGCTGAATGCTGCACCTTAATGTTCTTAACCGGCTTGTCTTAATGTGTG 360  
 Qy 121 LysIleAlaThrPheThrHisProValPhePheThrLeuLysHisLysLeuSerGlyTyr 140  
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 Qy 201 ThrTyrThrMetProThrAlaValPhePheIleCysMetIleLeuLeuIleThrSerLeu 220  
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 Qy 221 GlyArgHisArgLysLysAlaLeuLeuThrThrSerGlyPheArgLysProSerValGln 240  
 Db 661 GGAAGACACATGAAGAAGGCTCTCTTAACAACCTCAGATTTCCAGAGACCCAGAGTGCAG 720  
 Qy 241 AlaHisIleLysAlaLeuAlaLeuLeuSerPheAlaMetLeuPheIleSerTyrPhe 260  
 Db 721 GCACACATTAAGGCTATAGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 780  
 Qy 261 LeuSerLeuValPheSerAlaAlaGlyIlePheProProLeuAspPheLysPheTyrVal 280  
 Db 781 CTGTCACTGGTGTTCAGTGTGCGAGATTTTTCACCTCTGCACTTAATTTCTGGGTG 840  
 Qy 281 TyrGlnSerValIleTyrLeuCysAlaAlaValHisProIleIleLeuLeuPheSerAsn 300  
 Db 841 TGGGAGTCAGTGAATTTATCTGTGTGCGAGCACTTCAACCCATCATTTCTTACCTTCAGCAAC 900  
 Qy 301 CysArgLeuArgAlaValLeuLysSerArgArgSerSerArgCysGlyThrPro 318  
 Db 901 CGCAGGCTGAGAGCTGTGTGAAGAGGTGCCGTTCTCAAGGTGTGGACACCT 954

RESULT 12  
 AY725022 957 bp DNA linear PRI 18-SEP-2004  
 LOCUS Macaca mulatta chromosome 7 taste receptor T2R56 gene, complete cds.  
 DEFINITION  
 ACCESSION AY725022  
 VERSION AY725022.1 GI:51989321  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Macaca mulatta (rhesus monkey)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
 Cercopithecinae; Macaca.  
 1 (bases 1 to 957)  
 Anne, F., Yoav, G., Orna, M. and Svante, P.  
 Evolution of bitter taste receptors in human and apes  
 Unpublished  
 JOURNAL  
 TITLE  
 REFERENCE  
 2 (bases 1 to 957)  
 Anne, F., Yoav, G., Orna, M. and Svante, P.  
 Direct Submission  
 TITLE

JOURNAL Submitted (12-AUG-2004) Genetics, Max-Planck Institute for  
 Evolutionary Anthropology, Deutscher Platz 6, Leipzig 04103,  
 Germany

FEATURES  
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ORIGIN  
 Alignment Scores:  
 Pred. No.: 3.85e-124 Length: 957  
 Score: 1480.00 Matches: 285  
 Percent Similarity: 92.77% Conservative: 10  
 Best Local Similarity: 89.62% Mismatches: 23  
 Query Match: 88.20% Indels: 0  
 DB: 9 Gaps: 0

US-10-628-464-2 (1-318) x AY725022 (1-957)

Qy 1 MetAsnGlyAspHisMetValLeuGlySerSerValThrAspLysAlaIleLeu 20  
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 Qy 21 ValThrIleLeuLeuLeuLeuArgLeuValAlaIleAlaGlyAsnGlyPheIleThrAla 40  
 Db 61 GTTATCATTTTACTCTTTTGTGCTGCTGTRGCAATAGCAGCAATGGCTTCACTGCT 120  
 Qy 41 AlaLeuGlyValGlnTyrValLeuArgArgMetLeuLeuProCysAspLysLeuVal 60  
 Db 121 GCTGGGTGGAGTGGAGTGGTACAGGGAACTGTGCTGTGATGATTAATGTT 180  
 Qy 61 SerLeuGlyValAspSerArgPheCysLeuGlnSerValValMetGlyLysThrIleTyrVal 80  
 Db 181 AGCTTAGGGGCTCTGCTCTTTTGTCTGCACTGGGTGTAATGGTAAGACCACTTAATGTT 240  
 Qy 81 PheLeuHisProMetAlaPheProTyrAsnProValLeuGlnPheLeuAlaPheGlnTyr 100  
 Db 241 TTCTTGATCCGACGGCTTCCCATACACCTGTACTGGGGTTTCTAGCTTCCAGTGG 300  
 Qy 101 AspPheLeuAsnAlaAlaThrLeuTyrSerSerThrTyrLeuSerValPheTyrCysVal 120  
 Db 301 GACTTGCTGAATGCTGCACCTTCTGTGCTTCTAGCTGCGTCACTGCTTAATGTGTG 360  
 Qy 121 LysIleAlaThrPheThrHisProValPhePheThrLeuLysHisLysLeuSerGlyTyr 140  
 Db 361 AAAATTCCTACCTTACCCACCTCTCTCTCTCTGCTTAAGCAACAAGTTGCTGAGTGG 420  
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 Qy 161 IleGlyAsnHisArgMetTyrGlnAsnTyrLeuArgAsnHisLysLeuGlnProTyrPheVal 180  
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 Qy 201 ThrTyrThrMetProThrAlaValPhePheIleCysMetIleLeuLeuIleThrSerLeu 220

Db 601 ACTTGACATGCCACCTGCTCTTTTCATTGACATGATTTTGCATCATCATCTCTG 660  
Qy 221 GLYARGHIEARGLYSALALEULEUTHThrSerGlyPheArgGluProSerValGln 240  
Db 661 GGAGACACATGGAGAGAGCTCTCTTCAACCTCAGAGATTCGAGAACCCAGTGGACG 720  
Qy 241 AlaHisIleValaleuleualaleuleuSerPheAlaMetLeuPheIleSerTyPhe 260  
Db 721 GCACAGCTAAAGGCTGCTGCTCTCTCTCTTCCATGCTCTTCACTCATCTGATTTTC 780  
Qy 261 LeuSerIleuValPheSerAlaAlaGlyIlePheProProLeuAspPheIlePheTyrVal 280  
Db 781 CTGTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840  
Qy 281 TrpGluSerValIleTyriLeuCySAAlaValHisProIleIleLeuLeuPheSerAen 300  
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Qy 301 CySAArgLeuArgAlaValleuLysSerArgArgSerSerArgCySAglYThrPro 318  
Db 901 CGCAGGCTGAGACTGTGCTGAGAGAGTGCCTTCCCTGAGAGTGCAGACACCT 954

RESULT 13  
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LOCUS AF532786 putative taste receptor TR35 gene, complete cds.  
DEFINITION AF532786  
ACCESSION AF532786.1 GI:30793623  
VERSION  
KEYWORDS

SOURCE Mus musculus (house mouse)  
ORGANISM

REFERENCE  
AUTHORS Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
TITLE 1 (base 1 to 966) Eukarya; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (base 1 to 966) Conte, C., Ebeling, M., Marcuz, A., Nef, P., and Andres-Barguin, P. J.  
Evolutionary relationships of the Tas2r receptor gene families in  
mouse and human

JOURNAL Physiol. Genomics 14 (1), 73-82 (2003)

MEDLINE 22709097

PUBMED 12734386

REFERENCE 2 (base 1 to 966)

AUTHORS Conte, C., Ebeling, M., Marcuz, A., Nef, P., and Andres-Barguin, P. J.

TITLE Direct Submission

JOURNAL Submitted (26-JUL-2002) Pharma Research Basel, F. Hoffmann-La Roche

124, Basel CH-4070, Switzerland

Location/Qualifiers

source

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SIFMSLLVSLVNHMKTFILASELSDWAQAHFKALPLSLSTVIFISCFLLVLS

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ORIGIN

Alignment Scores:

Pred. No.: 3e-77  
Score: 960.00  
Percent Similarity: 73.70%

Best Local Similarity: 58.77% Mismatches: 81  
Query Match: 57.21% Indels: 0  
DB: 10 Gaps: 0

US-10-628-464-2 (1-318) x AF532786 (1-966)

Qy 1 MetAsnGlyAspHisMetValLeuGlySerSerValThrAspLysLysAlaIleIleLeu 20  
Db 28 ATGACACAGGCCATGACAGTCTTGATGTGACAGTACTGATGATGACAGTCTGACCTTA 87  
Qy 21 ValThrIleLeuLeuLeuLeuLysValAlaIleAlaGlyAsnGlyPheIleThrAla 40  
Db 88 TTTATCATTTTATGCTCTTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 147  
Qy 41 AlaLeuGlyValGluTrpValLeuArgAspMetLeuProCysAspLysLeuVal 60  
Db 148 GCACGTGGCATGAAAGTGTGCTCCGAGAAACACTGTCACTCATATATGATGATGATG 207  
Qy 61 SerLeuGlyAlaSerArgPheCysLeuGlnSerValValMetGlyLysThrIleTyVal 80  
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Qy 81 PheLeuHisProMetLysPheProTyraenProValLeuGlnPheLeuAlaPheGlnTrp 100  
Db 268 TTCCTGATATCAACAAGCTTCCATCAACCTGTAATACAGTCTCTTAATTAATGATG 327  
Qy 101 AspPheLeuAsnAlaIleThrLeuTrpSerSerThrTrpLeuSerValPheTyrcysVal 120  
Db 328 GACTTCTTACGTGCTGACCAACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 387  
Qy 121 LysIleAlaIleThrPheThrHisProValPhePheTrpLeuLysHisLysLeuSerGlyTrp 140  
Db 388 AAATATGCAACCTTAACCATCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 447  
Qy 141 LeuProTrpMetLeuPheSerSerValGlyLeuSerSerPheThrIleLeuPhePhe 160  
Db 448 GATCAACGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 507  
Qy 161 IleGlyAsnHisArgMetTyrcyGlnAsnTyrcyLeuArgAsnHisIleLeuGlnProTrpAenVal 180  
Db 508 ATGAGCAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 567  
Qy 181 ThrGlyAspSerIleArgSerTyrcyGlyLysPheTyrcyLeuPheProLeuLysMetIle 200  
Db 568 ACTGGAAATAGCTTAAGACATCACTGAGAAATTTCTACTCTTTCTTAATAAGATAATC 627  
Qy 201 ThrTrpThrMetProThrAlaValPhePheIleCysMetIleLeuLeuIleThrSerLeu 220  
Db 628 ATGTGACAAATCCCATCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 687  
Qy 221 GLYARGHIEARGLYSALALEULEUTHThrSerGlyPheArgGluProSerValGln 240  
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Db 808 CTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 867  
Qy 281 TrpGluSerValIleTyriLeuCySAAlaValHisProIleIleLeuLeuPheSerAen 300  
Db 868 TGGCAGGTGTGATTTATCTGTGACACAGATACATCCATGTTTATCTTTCAGCAAC 927  
Qy 301 CySAArgLeuArgAlaValleuLys 308  
Db 928 CCTGTTTGAGAGTGTGATTAAG 951

RESULT 14  
AC117625 203639 bp DNA linear HTG 13-MAR-2004  
LOCUS

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: February 4, 2005, 18:42:27 ; Search time 617 Seconds

(without alignments)  
3051.017 Million cell updates/sec

Title: US-10-628-464-2

Perfect score: 1678

Sequence: 1 NMGDHVLSSVTDKKAIL.....SNCRLAVALKSRSSRCGRP 318

Scoring table:

BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

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-Q=/cgn2.1/USPTO.spool/US10628464/runcat\_04022005\_115947\_4317/app\_query.fasta\_1.455  
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-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blonsum62 -TRANS=human40.cdi  
-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15  
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Database :

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2: geneseqn1990s: \*  
3: geneseqn2000s: \*  
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10: geneseqn2003cs: \*  
11: geneseqn2003ds: \*  
12: geneseqn2004as: \*  
13: geneseqn2004bs: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1678	100.0	954	6	ABK87584 DNA encod
2	1678	100.0	957	12	ADJ87104 Nucleotid
3	1678	100.0	957	13	ADM33336 Human bit
4	960	57.2	939	8	ACC44449 Gene enco
5	609	36.3	924	6	AAS18172 Human T2R

6	609	36.3	924	6	AB243209	Ab243209 Human GPC
7	609	36.3	924	13	ADR29249	ADR29249 Taste rec
8	609	36.3	1324	10	ADC6988	ADC6988 Human GPC
9	608	36.2	921	13	ADM33294	ADM33294 Human bit
10	600.5	35.8	9437	5	AAF92567	AAF92567 Mouse T2R
11	600.5	35.8	9437	13	ADR29217	ADR29217 Taste rec
12	593.5	35.4	1295	5	AAF92539	AAF92539 Rat T2R12
13	593.5	35.4	1295	13	ADR29161	ADR29161 Taste rec
14	425	25.3	885	8	ACC44453	ACC44453 Gene enco
15	416	24.4	873	13	ADM33330	ADM33330 Human bit
16	409	24.4	897	8	ACC44450	ACC44450 Gene enco
17	408	24.3	876	5	AAF92516	AAF92516 Human T2R
18	408	24.3	876	12	ADJ84512	ADJ84512 Human T2R
19	408	24.3	876	13	ADR29092	ADR29092 Taste rec
20	402.5	24.0	882	8	ACC44448	ACC44448 Gene enco
21	380	22.6	2887	5	AAF92559	AAF92559 Mouse T2R
22	380	22.6	2887	13	ADR29201	ADR29201 Taste rec
23	378.5	22.6	954	12	ADJ84495	ADJ84495 Human T2R
24	378.5	22.6	954	13	ADM33318	ADM33318 Human bit
25	378.5	22.6	957	12	ADQ17198	ADQ17198 Human sof
26	378.5	22.6	957	12	ADQ21802	ADQ21802 Human sof
27	378.5	22.6	957	12	ADQ17321	ADQ17321 Human sof
28	378.5	22.6	957	13	ADR29075	ADR29075 Taste rec
29	375.5	22.4	957	5	AAF92508	AAF92508 Human T2R
30	359	21.4	936	13	ADM33322	ADM33322 Human bit
31	359	21.4	939	5	AAF92510	AAF92510 Human T2R
32	359	21.4	939	12	ADJ84499	ADJ84499 Human T2R
33	359	21.4	939	13	ADR29079	ADR29079 Taste rec
34	356	21.2	914	12	ADJ84453	ADJ84453 Rat T2R03
35	356	21.2	6552	5	AAF92530	AAF92530 Rat T2R03
36	356	21.2	6552	13	ADR29143	ADR29143 Taste rec
37	345.5	20.6	939	8	ACC44451	ACC44451 Gene enco
38	344.5	20.5	1304	5	AAF92533	AAF92533 Rat T2R06
39	344.5	20.5	1304	13	ADR29149	ADR29149 Taste rec
40	341.5	20.4	957	12	ADQ22066	ADQ22066 Human sof
41	339	20.2	966	6	AAS18165	AAS18165 Human T2R
42	339	20.2	966	13	ADR29235	ADR29235 Taste rec
43	339	20.2	1017	6	AB243207	AB243207 Human GPC
44	339	20.2	1366	10	ADC87278	ADC87278 Human GPC
45	339	20.2	1417	10	ADC87332	ADC87332 Human GPC

## ALIGNMENTS

RESULT 1	ABK87584	standard; cDNA; 954 BP.
ID	ABK87584	
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AC	ABK87584:	
DT	24-SEP-2002	(first entry)
XX		
DE	DNA encoding novel human G-protein coupled receptor.	
XX		
KW	G-protein coupled; receptor; liver; central nervous system disease;	
KW	Alzheimer's disease; anorexia; dementia; metabolic disease; diabetes;	
KW	hyperlipemia; cancer; non-small cell lung cancer; ovarian cancer;	
KW	stomach cancer; breast cancer; colon cancer; bladder cancer; rheumatism;	
KW	circulatory disease; hypertension; atherosclerosis; angina; allergy;	
KW	inflammatory disease; respiratory disease; asthma; bronchitis;	
KW	digestive disease; stomach ulcer; duodenal ulcer; immune disorder;	
KW	autoimmune disease; infection; acquired immunodeficiency syndrome; AIDS;	
KW	pneumonia; influenza; gene; ss.	
XX		
OS	Homo sapiens.	
XX		
FH	Key	Location/Qualifiers
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FT		/product= "Novel G-protein coupled receptor"
FT		/partial
FT		/note= "No stop codon given"

PN WO200257309-A1.  
 XX  
 PD 25-JUL-2002.  
 XX  
 PF 17-JAN-2002; 2002WO-JP000271.  
 XX  
 PR 18-JAN-2001; 2001JP-00010814.  
 XX PR 30-MAR-2001; 2001JP-00102558.  
 XX  
 PA (TAKE ) TAKEDA CHEM IND LTD.  
 XX  
 PI Miwa M, Ico T, Shintani Y, Miyajima N;  
 DR WPI; 2002-538457/57.  
 DR P-PSDB; AAU98514.  
 XX  
 PT New G-protein coupled receptor protein expressed in human liver for  
 PT design of drugs and reagents for treatment and diagnosis of cancer and  
 PT respiratory metabolic and other diseases.  
 XX  
 PS Claim 6; Page 91; 101pp; Japanese.  
 XX  
 CC The invention describes a novel G-protein coupled receptor protein  
 CC expressed in human liver. The protein is used in the treatment,  
 CC prevention and diagnosis of central nervous system diseases (such as  
 CC Alzheimer's, anorexia and dementia), metabolic diseases (such as diabetes  
 CC and hyperlipaemia), cancer (such as non-small cell lung cancer, ovarian  
 CC cancer, stomach cancer, breast cancer, colon cancer and bladder cancer),  
 CC circulatory diseases (such as hypertension, atherosclerosis and angina),  
 CC inflammatory diseases (such as allergy and rheumatism), respiratory  
 CC diseases (such as asthma and bronchitis), digestive diseases (such as  
 CC stomach ulcer and duodenal ulcer), immune disorders (such as autoimmune  
 CC diseases), and infections (such as acquired immunodeficiency syndrome  
 CC (AIDS), pneumonia and influenza). This sequence encodes the novel G-  
 CC protein coupled receptor protein described in the invention  
 XX  
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 XX  
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 Pred. No.: 1 04e-160 Length: 954  
 Score: 1678.00 Matches: 318  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 6 Gaps: 0  
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 DB 1 ATGAATGGAGACCAATGGTTTAGGATCTTCGCTGACTGACAAAGGCATCATCTTG 60  
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 DB 61 GTTACCAATTTTACTCTTTTACCCCTGGTAGCAATAGCAGCAATGGCTTCATCACTGCT 120  
 QY 41 AlaLeuGIyValGIuTrpValLeuArgSerMetLeuLeuProCysAspIySlyLeuVal 60  
 DB 121 GCTCTGGGCGCTGGAGTGGGCTGCTACGAGAAATGTTGCTTGCTTGATTAAGTTAGGTT 180  
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 DB 181 AGCCTTAGGGGCGCTCTGCTCTGCTGCACTGAGTGTATGGGTAAAGACATTTATGTT 240  
 QY 81 PheLeuHisProMetAlaPheProTyArgProValLeuGIyPheLeuAlaPheGIyTrp 100  
 DB 241 TTCCTGCATCCGATGGGCTTCCCATACACCCTGTACTGAGATTTCTAGCTTCCAGTGG 300  
 QY 101 AspPheLeuAsnAlaIleThrLeuTrpSerSerThrTrpLeuSerValPheTyrcysVal 120  
 DB 301 GACTCTCTGAATGTGACACCTTATGGTCTCTTACCTGGCTGAGTGTCTTATGTGTG 360  
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 QY 141 LeuProThrMetLeuPheSerSerValGIyLeuSerSerPheThrThrIleLeuPhePhe 160  
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 QY 161 IleGIyAsnHisArgMetTyrcyIleAsnTyrcyLeuArgAsnHisLeuGIyProThrAsnVal 180  
 DB 481 ATAGGCAACACAGATGTATCAGAACTTTTAAAGAAACATCTAACACTTGGAAATGTC 540  
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 DB 541 ACTGGCGATAGCATACGAGACTGCTGAGAAATTTCTATCTCTTCCCTTAAAAATGATT 600  
 QY 201 ThrTrpThrMetProThrAlaValPhePheIleCysMetIleLeuLeuIleThrSerLeu 220  
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 QY 221 GIyArgHisArgIySlySlyAlaLeuLeuThrThrSerGIyPheArgGIyProSerValGIy 240  
 DB 661 GGAAGCACAGAAAGAGCTCTCTTACACCTGACATTCGAGAGCCAGTGGCAG 720  
 QY 241 AlaHisIleIyAlaIleuValAlaLeuLeuSerPheAlaMetLeuPheIleSerTyrcyPhe 260  
 DB 721 GCACACATAAAGGCTCTGCTGCTCTCTCTTTTGGCATGCTCTTCATCTCATATTTC 780  
 QY 261 LeuSerLeuValPheSerAlaIleGIyIlePheProProLeuAspPheIySlyPheTrpVal 280  
 DB 781 CTGTCACTGCTGTCTGCTCAGTCTCAGATATTTTCCACCTTGACCTTTAAATCTGGGTG 840  
 QY 281 TrpGIySerValIleTyrcyLeuCysAlaAlaValHisProIleIleLeuLeuPheSerAsn 300  
 DB 841 TGGAGTCACTGATATTATCTGTGTGACAGATTACCCCATCATTTGCTCTTCAGCAAC 900  
 QY 301 CysArgLeuArgAlaValLeuIySerArgArgSerSerArgCysGIyThrPro 318  
 DB 901 TCGAGGCTGAGAGCTGTGCTGGAAGATCCGCTTCTCTCAAGGTGTGGGACACT 954  
 RESULT 2  
 ADJ87104  
 ID ADJ87104 standard; DNA; 957 BP.  
 XX  
 AC ADJ87104;  
 XX  
 DT 06-MAY-2004 (first entry)  
 XX  
 DE Nucleotide sequence of human bitter taste receptor T2R76.  
 XX  
 KM Human; bitter taste receptor ; T2R76; chromosome 7; bitter taste ; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 1..957  
 FT /product= "bitter taste receptor T2R76"  
 XX  
 PN MO2004011617-A2.  
 XX  
 PD 05-FEB-2004.  
 XX  
 PF 29-JUL-2003; 2003WO-US023604.  
 XX  
 PR 29-JUL-2002; 2002US-0398727P.  
 XX  
 PA (SENO-) SENOMYX INC.  
 PA (ADLER/) ADLER J E.  
 PA (TANG/) TANG H.  
 PA (PRONIN/) PRONIN A.  
 PA (ZOLLER/) ZOLLER M.  
 PI Adler JE, Tang H, Pronin A, Zoller M;



XX WPI: 2004-143845/14.  
 DR P-PSDB; ADJ87105.  
 PT Novel isolated bitter taste receptor, T2R76 polypeptide useful for  
 PT identifying modulators of taste perception, or bitter compounds.  
 XX  
 PS Claim 1; Page 97-98; 100pp; English.  
 CC The present sequence encodes human bitter taste receptor T2R76. The human  
 CC T2R76 gene is located on chromosome 7 in the region 14q062692-14q063448.  
 CC The reading frame of T2R76 is intronless. T2R76 polypeptides and  
 CC polynucleotides are useful for identifying modulators. Such modulators  
 CC are useful for modulating bitter taste perception in a subject. T2R76  
 CC agonists can be administered to enhance bitter tastes, while T2R76  
 CC antagonists can be administered to reduce bitter taste.  
 XX  
 SQ Sequence 957 BP; 203 A; 241 C; 215 G; 298 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 1 05e-160 Length: 957  
 Score: 1678.00 Matches: 318  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 12 Gaps: 0  
 US-10-628-464-2 (1-318) x ADJ87104 (1-957)  
 QY 1 MetAaNgLyAspHisMetValLeuGlySerSerValThrAspLySAlaIleLeu 20  
 Db 1 ATGATGAGAGACCAAGTCTTCTAGATCTTCGGTGAAGCAAGAGCCATCATCTTG 60  
 QY 21 ValThrIleLeuLeuLeuLeuArgLeuValAlaIleAglYasNgLyPheIleThAla 40  
 Db 61 GTTACCAATTTTACTCTTTTACCGCTGTGACATACAGGCAATGCGCTTCATCATCTG 120  
 QY 41 AlaLeuGlyValAlaGluTPrpValLeuArgArgMetLeuLeuProCysAspLySLeuVal 60  
 Db 121 GCTCTGGGCGGTGGAGTGGGTCTAGAGAAAGTGTGCTGTGTGAATGATATTTGCTT 180  
 QY 61 SerLeuGlyAlaSerArgPheCysLeuGlnSerValValMetGlyLysThrIleTyrVal 80  
 Db 181 AGCTTAGGGGCTCTCGCTTCTGTCTGACGACATGGAATGGGTAGACCATTTATGTT 240  
 QY 81 PheLeuHisProMetAlaPheProTyrAsnProValLeuGlnPheLeuAlaPheGlnTyr 100  
 Db 241 TTCTTGCATCCGATGGCTTCCCATACACCTGTACTGACGTTTCTTAGCTTTCAGTGG 300  
 QY 101 AspPheLeuMetAlaAlaThrLeuTyrSerSerThrTyrLeuSerValPheTyrCysVal 120  
 Db 301 GACTTCTGAAATGTGCACCTTAAATGATGCTTAACTGCGACATGCTTCTTATTTGTG 360  
 QY 121 LysIleAlaThrPheThrHisProValPhePheTyrLeuLysHisLysLeuSerGlyTyr 140  
 Db 361 AAAATTCTTACCTTACCCACCTGCTCTTCTTCTGCTAAAGCAAGTGTCTCGGGTGG 420  
 QY 141 LeuProTyrMetLeuPheSerSerValGlyLeuSerSerPheThrThrIleLeuPhePhe 160  
 Db 421 CTACACATGATGCTCTTCAAGCTGTAGGGCTTCCAGCTTCCACACCATTTCTTTTTC 480  
 QY 161 IleGlyAsnHisAspMetTyrGlnAsnTyrLeuArgAsnHisLeuGlnProTyrAsnVal 180  
 Db 481 ATAGGCAACCAAGAAATGATCAACACTATTAAAGAAACCACTTCAACACCTTGAATGTC 540  
 QY 181 ThrGlyAspSerIleArgSerTyrCysGlyLysPheTyrLeuPheProLeuLysMetIle 200  
 Db 541 ACTGGCATATGACATACGAGTACTGTGAGAAATTCATCTCTTCCCTTAAATAATGATT 600  
 QY 201 ThrTyrThrMetProThrAlaValPhePheIleCysMetIleLeuLeuIleThSerLeu 220  
 Db 601 ACTTGGAACAATGCCACATGCTGTCTTTTCTTTTCTTGTGATGATTTGTCATCATCTCTG 660

QY 221 GlyArgHisArgLysLysAlaLeuLeuThrThrSerGlyPheArgLysProSerValGln 240  
 Db 661 GGAAGACACAGAAAGAAAGGCTCTCTTACCACTCGAGATCCGAGAGCCCACTGTGAG 720  
 QY 241 AlHisIleLysAlaLeuLeuAlaLeuLeuSerPheAlaMetLeuPheIleSerTyrPhe 260  
 Db 721 GCACACATAAAGGCTGCTGCTCTCTCTCTTTTGCATGCTTTCATCATATTTTC 780  
 QY 261 LeuSerLeuValPheSerSerAlaIleArgIlePheProProLeuAspPheLysPheThrVal 280  
 Db 781 CTGTCACTGTGTGTCTGAGTGTGAGATTTTTCACCTTGAACCTTAAATTTCTGGGTG 840  
 QY 281 TyrGlySerValIleTyrLeuCysAlaAlaValHisProIleIleLeuLeuPheSerAsn 300  
 Db 841 TGGGAGTCATGATTTTATCTGTGTGACAGAGTTCACCCCATCATTTGCTTCTCAGCAAC 900  
 QY 301 CysArgLeuArgAlaValLeuLysSerArgArgSerSerArgCysGlyThrPro 318  
 Db 901 TGCAGCTGAGAGCTGTGTGAAAGAGTCCGCTTCCATGAGTGTGGACACCT 954  
 RESULT 3  
 ADM3336  
 ID ADM3336 standard; cDNA; 957 BP.  
 XX  
 AC ADM3336;  
 XX  
 DT 18-NOV-2004 (first entry)  
 XX  
 DE Human bitter taste receptor TAS2R60 encoding cDNA SEQ ID NO:50.  
 XX  
 KM human; bitter taste receptor; food; gene; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 1..957  
 FT /\*lag= a  
 FT /product= "bitter taste receptor hTAS2R60"  
 XX  
 PN WC0204029087-A2.  
 XX  
 PD 08-APR-2004.  
 XX  
 PF 25-SEP-2003; 2003W0-EP010691.  
 XX  
 PR 25-SEP-2002; 2002JUS-0413298P.  
 XX  
 PA (DBER-) DEUT INST ERNAHRUNGSFORSCHUNG POTSDAM.  
 XX  
 PI Bufo B, Hofmann T, Krautwurst D, Kuhn C, Meyerhof W;  
 XX  
 DR WPI: 2004-305149/28.  
 DR P-PSDB; ADM3335.  
 XX  
 PT Novel bitter receptor polynucleotide encoding human TAS2R protein having  
 PT bitter substance binding activity, useful for producing nutraceutical or  
 PT pharmaceutical compositions comprising antagonists of bitter taste  
 PT receptor activity.  
 XX  
 XX Claim 14; SEQ ID NO 50; 108pp; English.  
 CC The present sequence encodes a human bitter taste receptor. Also  
 CC described: (1) a polynucleotide encoding a bitter taste receptor (I); (2)  
 CC a vector (II) containing (I); (3) a host cell (III) genetically  
 CC engineered with (I) or (II); (4) a transgenic non-human animal (IV)  
 CC containing (I), (II) and/or (III); (5) a polypeptide (V) having the amino  
 CC acid sequence encoded by (I) or obtained by culturing (III) and  
 CC recovering polypeptide; (6) an antibody (VI) specifically binding to (V);  
 CC (7) a nucleic acid molecule (VII) specifically hybridizing to (I); (8) an  
 CC antagonist/inhibitor (VIII) against (V) which is antibody, the  
 CC extracellular domain of (V) or its fragment or an inhibiting RNA; (9)  
 CC isolating (M1) a compound that binds to (V) encoded by (I); (10)  
 CC isolating (M2) an antagonist of bitter taste receptor activity; (11) a

CC foodstuff including human and animal foodstuff, any precursor material or  
 CC additive employed in the production of foodstuff comprising (VIII); and  
 CC (12) a nutraceutical/pharmaceutical composition comprising (VII); and an  
 CC active agent and optionally a carrier. (III) is useful for producing a  
 CC polypeptide encoded by (I), which involves culturing (III) and recovering  
 CC the polypeptide encoded by (I). (II) is useful for producing cells  
 CC capable of expressing at least one of the bitter taste receptor  
 CC polypeptide, which involves genetically cells in vitro with (II), where  
 CC the bitter taste receptor polypeptide(s) is/are encoded by (I). (M1) or  
 CC (M2) can be used for producing food or any precursor material or additive  
 CC employed in the production of foodstuffs. (M1) or (M2) can also be used  
 CC for producing nutraceutical or pharmaceutical compositions. (I), (II),  
 CC (VI) or (VIII) can be used for manufacturing a medicament for the  
 CC treatment of an abnormally increased or decreased sensitivity towards a  
 CC bitter substance. The identified agonist/inhibitor efficiently suppresses  
 CC or eliminates bitter tasting components of food and effectively useful in  
 CC food industries.

XX Sequence 957 BP; 203 A; 240 C; 215 G; 299 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.:	1.05e-160	Length:	957
Score:	1678.00	Matches:	318
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	13	Gaps:	0

US-10-628-464-2 (1-318) X ADM3336 (1-957)

QY 1 MetAenGIYAAPHISmetValLeuGIYSeSerValThraAPlyblyAlaIlelleu 20  
 DB 1 ATGAATGAGACCAACATGTTCTAGGATCTTCGCTGACTGACAAGAGCCATCATCTTG 60  
 QY 21 ValThrIleuLeuLeuLeuAryleuValAlaIlelleuGIYblyPheIleThrAla 40  
 DB 61 GTTACCATTTTACTCTTTTACCGCTGTAGCAATAGCAGCAATGGCTTCATCAGCTGCT 120  
 QY 41 AlaLeuGIYValGIUTPValLeuAryGmetLeuLeuProCYaAPlyblyLeuLeuVal 60  
 DB 61 GTTACCATTTTACTCTTTTACCGCTGTAGCAATAGCAGCAATGGCTTCATCAGCTGCT 120  
 QY 121 GCCTCTGGGCTGAGAGTGGCTGACGAGAAATGTTGGCTTGTATTAAGTTATGGTT 180  
 DB 61 SerLeuGIYAlaSerAryPheCYLeuGIYSeSerValValMetGIYblyThrIleYrVal 80  
 DB 181 AGCTTAGGGGCTCTGCTCTCTGCTGACATGAGTGTATAGGTAAGACCATTTATGTT 240  
 QY 81 PheLeuHISerMetAlaPheProTYrAanProValleuGIYblyPheLeuAlaPheGIYTrp 100  
 DB 241 TTCTTGATCTCGAATGGCTTCCATACACCTGAGTGAAGTTTCTTACGTTTCCAGTGG 300  
 QY 101 AspPheLeuAanAlaAlaThrLeuTrpSerSerThrTrpLeuSerValPheTYrCYVal 120  
 DB 301 GACTTCTGATGCTGACACCTTATGTTCTTACCTGCTGACGTGCTTCTTATTTGTTG 360  
 QY 121 LysIleAlaThrPheThrHisProValPhePheTrpLeuYshIshIshLeuSerGIYTrp 140  
 DB 361 AAATATGCTACCTTACCCACCTGCTTCTTCTGCTTAAGACAAAGTTGCTGGGTGG 420  
 QY 141 LeuProTrpMetLeuPheSerSerValGIYLeuSerSerPheThrTrpIleLeuPhePhe 160  
 DB 421 CTACCATGATGCTTCTGACCTGTAGGGCTCTCCAGCTTCCACCATTTCTATTTTTC 480  
 QY 161 IleGIYAanHisAryMetTYrGIYAsnTYrLeuAryGanHisIshleuGIYProTPAanVal 180  
 DB 481 ATAGGCAACACAGAAATGATCAGAACTATTAAAGAACATCTACAACTTGGAAATGTC 540  
 QY 181 ThrGIYAasSerIleArgSerTYrCYGIYblyPheTYrLeuPheProLeuYshMetIle 200  
 DB 541 ACTGGGATGATGATACGAGACTACTGAGAAATTTCTATCTTCCCTTAATAAATGATT 600  
 QY 201 ThrTrpThrMetProThrAlaValPhePheIleCYshMetIleLeuLeuIleThrSerLeu 220  
 DB 601 ACTTGACAAATGCCACTGCTGCTTCTTTTCAATTTGCAATTTTGTCTATCACATCTCTG 660

QY 221 GIYArGHISarGIYblyblyAlaLeuLeuThrTrpSerGIYblyPheArgGIYProSerValGIY 240  
 DB 661 GGAGAGCACAGGAAGAGGCTCTCCCTTACACTGAGTATCCGAGAGCCAGTGGCAG 720  
 QY 241 AlaHISIleLysAlaLeuLeuAlaLeuLeuSerPheAlaMetLeuPheIleSerTYrPhe 260  
 DB 721 GGACACATTAAGGCTCTGCTGCTCTCCCTTCTTGGCATATCTTCTTCAATCATATTTC 780  
 QY 261 LeuSerLeuValPheSerAlaIleGIYIlePheProProLeuAanPheYshPheTrpVal 280  
 DB 781 CTGTCACTGCTGTCTGCTGCTGAGTATTTTTCACCTTGACTTAAATTCGGGGTG 840  
 QY 281 TrpGIYSeSerValIleTYrLeuCYAlaAlaValHisProIleIleLeuLeuPheSerAan 300  
 DB 841 TGGAGATCATGATTTATCTGTGTGAGCAGATTACCCCATCATTTCTGCTTTCAGCAAC 900  
 QY 301 CYArGIYLeuAryAlaValLeuLysSerAryArgSerSerAryCYAGIYThrPro 318  
 DB 901 TGCAGGCTGAGAGCTGTGCTGAAGAGTCTGCTTCTTCAAGGTGTGGACACT 954

## RESULT 4

ACCA4449  
 ID ACC4449 standard; DNA; 939 BP.  
 XX  
 AC ACC4449;  
 XX  
 XX  
 DT 25-JUL-2003 (first entry)  
 XX  
 DE Gene encoding mouse GI endocrine cell specific GPCR G2R-m39.  
 XX  
 KM Chemosensor; G-protein coupled receptor; gene; ds; GPCR; receptor;  
 KM gastrointestinal tract; taste; ion channel; enteroendocrine cell.  
 XX  
 OS Mus musculus.  
 PN WO2003031604-A1.  
 XX  
 PD 17-APR-2003.  
 XX  
 PF 11-OCT-2002; 2002MO-US032664.  
 XX  
 PR 12-OCT-2001; 2001US-0328933P.  
 XX  
 PA (REGC) UNIV CALIFORNIA.  
 PA (PHLE/) PHLEGER C S W.  
 XX  
 XX Walsh JH, Rozengurt JE, Wu SV;  
 XX  
 DR P-PSDB; ABR58013.  
 DR  
 PT New nucleic acid encoding a chemosensing G-protein coupled receptor  
 PT useful for identifying chemical sensing receptors and signaling molecules  
 PT that allow pharmacological and genetic modulation of taste transduction  
 PT pathways.  
 PS Claim; Page 63; 101pp; English.  
 XX  
 CC This sequence represents a gene encoding a novel isolated chemosensing G-  
 CC protein coupled receptor (GPCR) from the gastrointestinal tract. The  
 CC nucleic acid is useful for identifying or isolating chemical sensing  
 CC receptors (including taste ion channels) and signaling molecules that  
 CC would allow pharmacological and genetic modulation of taste transduction  
 CC pathways. The native STC-1 enteroendocrine cells that naturally express  
 CC G2R are useful in identifying modulators of taste receptor-mediated  
 CC signal transduction. These cells are also used as models for studying  
 CC taste-mediated signal transduction  
 CC  
 SO Sequence 939 BP; 224 A; 209 C; 202 G; 304 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.: 1.01e-87 Length: 939

Score: 960.00 Matches: 181  
 Percent Similarity: 73.70% Conservative: 46  
 Best Local Similarity: 58.77% Mismatches: 81  
 Query Match: 57.21% Indels: 0  
 DB: 8 Gaps: 0

US-10-628-464-2 (1-318) x ACC44449 (1-939)

QY 1 MetAsnGlyAspHisMetValLeuGlySerSerValThrAspValValAlaIleLeu 20  
 DB 1 ATAGCAGCAGGCGCATCTTCTTGATGTGACATCTGATTAAGACAGTGCACCTTA 60  
 QY 21 ValThrIleLeuLeuLeuLeuArgLeuValAlaIleValGlyAsnGlyPheIleThrAla 40  
 DB 61 TTTATCATTTTATGCTCTTTTGTGCTGTGCGAGGTGTAGCAATGATTTATCATTTATA 120  
 QY 41 AlaleuGlyValGluTrpValLeuArgArgMetLeuLeuProCysAspValSleuLeuVal 60  
 DB 121 GCACTGGGCAATGAATGTTGCTCCGAGAACATGTCAGCTCATTAATTAAGTTACTGATC 180  
 QY 61 SerLeuGlyAlaSerArgPheCysLeuGlnSerValValMetGlyValThrIleTrpVal 80  
 DB 181 AGCTACACCCCTCTCATCTGTCTCAATGTGTGTGAATGAATATTTATGTT 240  
 QY 81 PheLeuHisProMetAlaPheProTrpAsnProValLeuGlnPheLeuAlaPheGlnTrp 100  
 DB 241 TTCTGATATCCACACAGCTTCCCATACACCTTATACAGCTCTTAATTTATATGTCG 300  
 QY 101 AspPheLeuAsnAlaAlaThrLeuTrpSerSerThrTrpLeuSerValPheTrpCysVal 120  
 DB 301 GACTCTTGACTGCTGCAACCATCTGCTGTTCTTGAGTTCTTATTTGTTG 360  
 QY 121 LysIleAlaThrPheThrIleAspProValPhePheTrpLeuValHisValSleuSerGlyTrp 140  
 DB 361 AAAATGTCAACCTTAACCATCTGCTGTTGCTGCTAAAGTACAGTGCCTGGGTGG 420  
 QY 141 LeuProTrpMetLeuPheSerSerValGlyLeuSerSerPheThrIleLeuPhePhe 160  
 DB 421 GTACCATGATGCTGCTCAAGTGTGTGGGATGTGAGCTTAAGTACTAATCTTATGTTTC 480  
 QY 161 IleGlyAsnHisArgMetCysGlnAsnTrpLeuArgAsnHisSleuGlnProTrpAsnVal 180  
 DB 481 ATAGGCAATTAATGATATATACAGACATGCAAAAGTGGCCATCACTTGAATGTC 540  
 QY 181 ThrGlyAspSerIleArgSerTrpCysGlnPheTrpLeuPheProLeuValMetIle 200  
 DB 541 ACTGGGAATGCTTAAGACACTCACTTGAGAAATTTCTTCTTCTTAATAAAGATATATC 600  
 QY 201 ThrTrpThrMetProThrAlaValPhePheIleCysMetIleLeuLeuIleThrSerLeu 220  
 DB 601 ATGTGGCAATCTCCACCTGTTGTTTCAGCATCTTCATGAGTTGCTCTCGTATCTTGG 660  
 QY 221 GlyArgHisArgLysLysAlaLeuLeuThrThrSerGlyPheArgGluProSerValGln 240  
 DB 661 GTAAGACACATGAAGAAGACTTCTTGCCCTTTCAGAACTTGGGATGTCTGGGCACAG 720  
 QY 241 AlaHisIleLysAlaLeuLeuAlaLeuLeuSerPheAlaMetLeuPheIleSerTrpPhe 260  
 DB 721 GCCCATTTCAAGGCTCTTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 780  
 QY 261 LeuSerLeuValPheSerAlaAlaGlyIlePheProProLeuAspPheValPheTrpVal 280  
 DB 781 CTGACGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840  
 QY 281 TrpGluSerValIleTrpLeuCysAlaAlaAlaValHisProIleIleLeuLeuPheSerAsn 300  
 DB 841 TGGAGAGTGTGATTCATCTGTGACAGTATACATCCCATTTGATATCTTACAGCAC 900  
 QY 301 CysArgLeuArgAlaValLeuLys 308  
 DB 901 CTTGTTTGGAGAGTGTGATTAAG 924  
 RESULT 5

AA818172  
 ID AA818172 standard; cDNA; 924 BP.  
 XX  
 AC AA818172;  
 XX  
 DT 26-MAR-2002 (first entry)  
 XX  
 DE Human T2R71 (hT2R71) cDNA.  
 XX  
 KW Human; T2R taste GPCR; taste cell-specific G protein-coupled receptor;  
 KW hT2R71; T2R71; T2R; bitter taste sensation; taste signaling pathway; ss;  
 KW taste transduction; food taste masking; drug taste masking.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 1..900  
 FT /tag= a  
 FT /product= "Human T2R71"  
 XX  
 PN NO200177676-A1.  
 XX  
 PD 18-OCT-2001.  
 XX  
 PF 04-APR-2001; 2001NO-US010739.  
 XX  
 PR 07-APR-2000; 2000US-0195532P.  
 PR 13-NOV-2000; 2000US-0247014P.  
 XX  
 PA (SENO-) SENOMYX INC.  
 XX  
 PI Adler JE;  
 XX  
 DR WPI; 2002-017486/02.  
 DR P-PSDB; AA011389  
 XX  
 PT Novel isolated mammalian taste cell-specific G protein-coupled receptor,  
 PT T2R, involved in bitter taste sensation; useful for identifying taste  
 PT modulators that are used to decrease or mask bitter taste of foods or  
 PT drugs.  
 XX  
 PS Claim 1; Page 74; 103bp; English.  
 XX  
 CC The invention relates to a mammalian taste cell-specific G protein-  
 CC coupled receptor (GPCR), T2R taste GPCR, involved in bitter taste  
 CC sensation. The T2R polypeptides and their associated polynucleotides are  
 CC useful for screening one or more compounds for the presence of taste  
 CC detectable by a mammal. Modulators of T2R polypeptides (modulators of  
 CC taste transduction) are useful for pharmacological and genetic  
 CC modulations of taste signaling pathways. These modulatory compounds are  
 CC then used in food and pharmaceutical industries to customise taste, e.g.,  
 CC to decrease or mask the bitter taste of foods or drugs. This sequence  
 CC represents cDNA encoding the human T2R71 (hT2R71) polypeptide  
 XX  
 SQ Sequence 924 BP; 180 A; 249 C; 214 G; 281 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 4.76e-52 Length: 924  
 Score: 609.00 Matches: 122  
 Percent Similarity: 57.73% Conservative: 46  
 Best Local Similarity: 41.92% Mismatches: 111  
 Query Match: 36.29% Indels: 12  
 DB: 6 Gaps: 2  
 US-10-628-464-2 (1-318) x AA818172 (1-924)  
 QY 21 ValThrIleLeuLeuLeuLeuArgLeuValAlaIleValGlyAsnGlyPheIleThrAla 40  
 DB 28 GTGTGCTCTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 87  
 QY 41 AlaleuGlyValGluTrpValLeuArgArgMetLeuLeuProCysAspValSleuLeuVal 60  
 DB 88 GTGCTGGGCAAGAGTGTGCTGCAATATGCAAGTGTGCTGCTTGTGATATGATCTCATTT 147

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QY 61 SerLeuGIyAlaSerArpPheCysLeuGlnSerValIvalMeGlyLysThrIleTyrVal 80
DB 148 AGCTTGGGTCCTCCCGCTTCTGCTGCACTGGTGGAGCGGTGACAACTTCTACTAC 207
QY 81 PheLeuHIsProMeAlaPheProTyrAraProValLeuGlnPheLeuAlaPheGlnTyr 100
DB 208 TCTGCCAAGAGTCACTCTGGGGGTCTCGGCCGACAGTCTTCCATCTACACTGG 267
QY 101 AspPheLeuAsnAlaIalThrLeuTyrPseSerThrTyrLeuSerValPheTyrCysVal 120
DB 268 CACTTCTTAACCTACACCACTTCTGCTGTTGGACGTGGCTGAGTCTCTGTTCTGTG 327
QY 121 LysIleAlaThrPheThrHisProValPhePheTyrLeuLysHisLeuSerGlyTyr 140
DB 328 AGATTGCTAACATCAACACCTCCACTTCTGCTGCTGAGTGAAGGAGGTTCCAGAGGTG 387
QY 141 LeuProTyrMeLeuPheSerSerValGlyLeuSerSerPheThrThrIleLeuPhePhe 160
DB 388 GTGCCCTGCTCTGTTGGGCTCTGCTGCTGATCTCTTCACTAACCCGTGTTT 447
QY 161 IleGlyAsnHisArgMetTyrGlnAsnTyrLeu-----ArgAsnHisLeu 175
DB 448 TGGGTGAACCTACCTGTATATCAAGATTATTAAGAAATTTTCTGGAAACATGACC 507
QY 176 GlnProTyrAsnValThrGlyAspSerIleArgSerTyrCysGlyLysPheTyrLeuPhe 195
DB 508 TACAACTGGAT-----ACAAGATAGAAACATCTATTTCCTCCCA 546
QY 196 ProLeuLysMetIleThrTyrThrMetProThrAlaValPhePheIleCysMetIleLeu 215
DB 547 TCCCTGAAACTGGTCACTGGTCAATCTTCTGTTTCTGTTTCTGATCAATTATGCTG 606
QY 216 LeuIleThrSerLeuGlyArgHisArgLysValAlaLeuLeuThrThrSerGlyPheArg 235
DB 607 TTAATTAATCTCTGAGAGGCACTGACTGAGAGATGACACAAACGGGCAACCTGACAG 666
QY 236 GluProSerValGlnIalHisIleLysValAlaLeuLeuAlaLeuLeuSerPheAlaMetLeu 255
DB 667 GACCCAGACCCAGGCTCACACAGAGCTGTAAGTCCCTCATCTCTTCCCATCTTT 726
QY 256 PheIleSerTyrPheLeuSerLeuValPheSerAlaAlaGlyIlePheProPheLeuAsp 275
DB 727 TATGCTCTGCTCTTCTGCTGCTGATCATGATGCGCAAAATTTATCTTCATGACAGAAC 786
QY 276 PheLysPheThrValTyrGlnSerValIleTyrLeuCysAlaIalValHisProIleIle 295
DB 787 GACTTTACTGGCCATGCGCAAAATGCAAGTCTACCTGTCATATCTGTCATCTCTTCATC 846
QY 296 LeuLeuPheSerAsnCysArgLeuArgAlaVal 306
DB 847 CTCATCTTCAACCACTCAAGCTTCCAGAGCTG 879

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RESULT 6
ABZ43209 ID ABZ43209 standard; DNA; 924 BP.
XX
XX ABZ43209;
AC
XX 06-MAR-2003 (first entry)
XX
XX Human GPCR polynucleotide SEQ ID NO 679.
DE
XX Human; GPCR; G protein coupled receptor; signal transduction; olfactory;
KW drug development; gustatory; taste; fragrance; gene; de.
XX
XX Homo sapiens.
OS
XX PN MO200216548-A2.
XX
XX 28-FEB-2002.
PD
XX 30-JUL-2001; 2001MO-IB001446.
PF

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XX 04-AUG-2000; 2000JP-00237818.
PR 13-FEB-2001; 2001JP-00034434.
XX
XX (NISC-) JAPAN SCI & TECHNOLOGY CORP.
XX
XX Haga T, Takeda S, Mitaku S;
PI
XX WPI; 2002-304118/34.
DR P-PDB; ABP95935.
XX
XX Database global search for G protein-coupled receptors, proteins and
PT encoded genes for studying in vivo signal transduction mechanism and
PT identifying targets for drug development.
XX
PS Claim 9; SEQ ID NO 679; 97pp + Sequence Listing; Japanese.
XX
XX The invention relates to a method for screening G protein-coupled
CC receptor (GPCR) genes (ABZ42870-ABZ43216) and/or GPCR proteins (ABP9596-
CC ABP95942) by extracting open-reading frames containing 6-8 transmembrane
CC domains with 250-1000 amino acid residues to give a gene homologous with
CC a known GPCR gene. The receptor proteins and encoded genes are useful for
CC studying in vivo signal transduction mechanism and identifying targets
CC for drug development e.g. based on olfactory and gustatory receptors in
CC form of agonists and antagonists by screening intrinsic and extrinsic
CC ligands as bitter taste inhibitors, taste enhancers and fragrance
CC improvers. Note: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 924 BP; 180 A; 249 C; 214 G; 281 T; 0 U; 0 Other;
SQ

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US-10-628-464-2 (1-318) x ABZ43209 (1-924)

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QY 161 IleGlyAsnHisArgMetTyrGlnAsnTyrLeu-----ArgAsnHisLeu 175
DB 448 TGGGTGAACCTACCTGTATATCAAGATTATTAAGAAATTTTCTGGAAACATGACC 507

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

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Run on: February 4, 2005, 20:02:23 ; Search time 209 Seconds

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2489.646 Million cell updates/sec

Title: US-10-628-464-2

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Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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2	418.5	24.9	4877	4 US-09-949-016-14084	Sequence 14084, A
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4	408	24.3	876	4 US-09-393-634-65	Sequence 65, Appl
5	408	24.3	876	4 US-09-949-016-1048	Sequence 1048, Ap
6	378.5	22.6	954	4 US-09-393-634-48	Sequence 48, Appl
7	378.5	22.6	957	4 US-09-949-016-3382	Sequence 3382, Ap
8	378.5	22.6	4957	4 US-09-949-016-15124	Sequence 15124, A
9	359	21.4	939	4 US-09-393-634-52	Sequence 52, Appl
10	358	21.3	12226	4 US-09-949-016-12237	Sequence 12237, A
11	356	21.2	1463	4 US-09-393-634-6	Sequence 6, Appl
12	337.5	20.1	930	4 US-09-393-634-50	Sequence 50, Appl

13	336.5	20.1	910	4 US-09-393-634-38	Sequence 38, Appl
14	336	20.0	900	4 US-09-393-634-36	Sequence 36, Appl
15	332.5	19.8	950	4 US-09-393-634-40	Sequence 40, Appl
16	332.5	19.8	951	4 US-09-949-016-2335	Sequence 2336, Ap
17	332.5	19.8	4951	4 US-09-949-016-14078	Sequence 14078, A
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28	273.5	16.3	924	4 US-09-393-634-54	Sequence 54, Appl
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36	203.5	12.1	819	4 US-09-393-634-10	Sequence 10, Appl
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41	177.5	10.6	601	4 US-09-949-016-38510	Sequence 38510, A
42	177.5	10.6	601	4 US-09-949-016-80952	Sequence 80952, A
43	176.5	10.5	601	4 US-09-949-016-108237	Sequence 108237, A
44	169	10.1	601	4 US-09-949-016-38861	Sequence 38861, A
45	169	10.1	601	4 US-09-949-016-78195	Sequence 78195, A

#### ALIGNMENTS

RESULT 1  
US-09-949-016-12790  
; Sequence 12790, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTNER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: C1001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; PRIOR FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 12790  
; TYPE: DNA  
; LENGTH: 4876  
; ORGANISM: Human  
US-09-949-016-12790  
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Pred. No.: 1.03e-39  
Score: 418.50  
Percent Similarity: 48.47%  
Best local Similarity: 30.06%  
Query Match: 24.94%  
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Gaps: 4  
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Sequence 14084, Application US/09949016  
Patent No. 6812339  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF.  
FILE REFERENCE: CL001307  
CURRENT APPLICATION NUMBER: US/09/949,016  
PRIOR FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSeq for windows Version 4.0  
SEQ ID NO 14084  
LENGTH: 4877  
TYPE: DNA  
ORGANISM: Human  
US-09-949-016-14084

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US-10-628-464-2 (1-318) x US-09-949-016-14084 (1-4877)

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

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Run on: February 4, 2005, 21:46:44 : Search time 618 Seconds

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Title: US-10-628-464-2

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Scoring table:

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

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8	609	36.3	924	18	US-10-724-208-17
9	600.5	35.8	924	17	US-10-292-798-1441
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27	378.5	22.6	954	17	US-10-364-861-48
28	362	21.6	939	18	US-10-723-860-14
29	359	21.4	939	9	US-09-393-634-52
30	359	21.4	939	10	US-09-510-332-18
31	359	21.4	939	16	US-10-383-982-52
32	359	21.4	939	17	US-10-364-861-52
33	356	21.2	914	17	US-10-364-861-6
34	356	21.2	1463	9	US-09-393-634-6
35	356	21.2	1463	16	US-10-383-982-6
36	356	21.2	6582	10	US-09-510-332-82
37	356	21.2	6582	18	US-10-723-860-14
38	344.5	20.5	1304	10	US-09-510-332-88
39	344.5	20.5	1304	18	US-10-723-860-14
40	341.5	20.4	957	18	US-10-723-860-14
41	339	20.2	966	9	US-09-825-882-3
42	339	20.2	966	18	US-10-724-208-3
43	339	20.2	966	18	US-10-724-208-3
44	339	20.2	966	18	US-10-724-208-3
45	339	20.2	1017	17	US-10-343-650A-675

#### ALIGNMENTS

RESULT 1  
US-10-628-464-1  
Sequence 1, Application US/10628464  
Publication No. US2004012134A1  
GENERAL INFORMATION:  
APPLICANT: ADLER, JON ELLIOT  
APPLICANT: TANG, HUIXIAN  
APPLICANT: PRONIN, ALEXEY  
TITLE OF INVENTION: IDENTIFICATION OF A NOVEL BITTER TASTE RECEPTOR, T2R76  
FILE REFERENCE: 100317.54260US  
CURRENT FILING DATE: 2003-07-29  
NUMBER OF SEQ ID NOS: 2  
SOFTWARE: PatentIn Ver. 3.2  
SEQ ID NO 1  
LENGTH: 957  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS

LOCATION: (1) . (954)  
US-10-628-464-1

## Alignment Scores:

Pred. No.:	1,32e-173	Length:	957
Score:	1678.00	Matches:	318
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
	18	Gaps:	0

US-10-628-464-2 (1-318) x US-10-628-464-1 (1-957)

```
QY 1 MetAsnGlyAspHisMetValLeuGlySerSerValThrAspIlyValIleLeu 20
Db 1 ATGAAGGAGACCAACATGGTTAGATCTTCGGTGACTACAGAAAGGCATCTTGG 60
QY 21 ValThrIleLeuLeuLeuLeuValGLeuValAlaIleAlaGlyAsnGlyPheIleThrAla 40
Db 61 GTTACCACTTTTACTCTTTTACCGCTGGTAGCAATAGCAAGCAATGGCTTCATCAGTGT 120
QY 41 AlaLeuGlyValAlaGluTrpValLeuArgArgMetLeuLeuProCysAspIlyLeuVal 60
Db 121 GCTCTGGCGTGAAGTGGGTGCTACGAGAAATGTTGCTTGATGAATAATTGGTT 180
QY 61 SerLeuGlyAlaSerArgPheCysLeuGlnSerValValMetGlyIlyThrIleTyVal 80
Db 181 AGCTTAGGGGCGCTCTGCTTCTGTCTGCACATGCTGTATAGGTAAGCACTTATAGTT 240
QY 81 PheLeuHisProMetAlaPheProTyArgProValLeuGlnPheLeuAlaPheGlnTrp 100
Db 241 TTTCTTGATCCGATGGCGCTTCCCATACMACCTGTACTGAGTTTCTTACGTTTCCAGTGG 300
QY 101 AspPheLeuLeuAlaAlaThrLeuTrpSerSerThrTrpLeuSerValPheTyArgVal 120
Db 301 GACTTCTGATAGCTGACCTTATGATGCTTACCTGCGCTGAGTCTTCTATGTTG 360
QY 121 LysIleAlaThrPheThrHisProValPhePheTrpLeuIlyHisIlyLeuSerGlyTrp 140
Db 361 AAAATGCTACCTTACCCACCCCGCTTCTTCTGCGTAAAGCAACAAGTTGCTGGGTGG 420
QY 141 LeuProTrpMetLeuPheSerSerValGlyLeuSerSerPheThrTrIleLeuPhe 160
Db 421 CTTCACATGATGCTTCTGCTGCTGTAGGGCTCTCCGCTTCCACCACTTCTATTTTTC 480
QY 161 IleGlyAspHisArgMetTyArgIleuTrpLeuArgAsnHisIleuGlnProTrpAsnVal 180
Db 481 ATAGGCAACCAAGAAATGATCAAGAACTATTAAAGAACATCTACAACTTGAATGTC 540
QY 181 ThrGlyAspSerIleArgSerTyCysGlyIlyPheTyLeuPheProLeuIlyMetIle 200
Db 541 ACTGGGATGACATAGGAGCTACTGTGAGAAATTCATCTTCCCTCTCAAAAATGATT 600
QY 201 ThrTrpThrMetProThrAlaValPhePheIleCysMetIleLeuLeuIleThrSerLeu 220
Db 601 ACTTGGACATAGCCCATCTGCTGCTTTTTCATTTGATTTGCTTCATCAATCTCTG 660
QY 221 GlyArgHisArgIlyValAlaLeuLeuThrThrSerGlyPheArgGluProSerValGln 240
Db 661 GGAAGACACAGAAAGAGCTTCTCTTACAACTTCAGAAATTCGAGAGGCCAGGTGACG 720
QY 241 AlaHisIleIlyValAlaLeuLeuAlaLeuLeuSerPheHisMetLeuPheIleSerTyPhe 260
Db 721 GCACACATAAAGGCTGCTGGGCTCTCTCTTTTGGCATGCTTCATCATATATTC 780
QY 261 LeuSerIleuValPheSerAlaAlaGlyIlePheProProLeuAspPheIlyPheTrpVal 280
Db 781 CTGTCACTGGTGTGTAGTGTGACAGGTATTTTCCACTTGGACCTTAAATCTCTGGGTG 840
QY 281 TrpGlySerValIleTyArgLeuCysAlaAlaValHisProIleIleLeuLeuPheSerAsn 300
Db 841 TGGGAGTCAATGATTTATCTGTGTGACAGAGTTCACCCCAATCTGCTTCCAGACAC 900
```

QY 301 CysArgLeuArgAlaValLeuIlySerArgArgSerSerArgCysGlyThrPro 318  
Db 901 TGCAGGCTGAGAGCTGTGCTGGAAGATGTCGTTCTCTCAAGGTGTGGACACT 954

## RESULT 2

US-09-825-882-17  
Sequence 17, Application US/09825882  
Patent No. US2002094551A1  
GENERAL INFORMATION:  
APPLICANT: ADLER, JON ELLIOT  
TITLE OF INVENTION: T2R TASTE RECEPTORS AND GENES ENCODING SAME  
FILE REFERENCE: 078003/0279152/RXT  
CURRENT APPLICATION NUMBER: US/09/825,882  
PRIOR FILING DATE: 2001-04-05  
PRIOR APPLICATION NUMBER: 60/195,532  
PRIOR FILING DATE: 2000-04-07  
PRIOR APPLICATION NUMBER: 60/247,014  
NUMBER OF SEQ ID NOS: 31  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 17  
LENGTH: 924  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-825-882-17

## Alignment Scores:

Pred. No.:	1.52e-56	Length:	924
Score:	609.00	Matches:	122
Percent Similarity:	57.73%	Conservative:	46
Best Local Similarity:	41.92%	Mismatches:	111
Query Match:	36.29%	Indels:	12
	9	Gaps:	2

US-10-628-464-2 (1-318) x US-09-825-882-17 (1-924)

```
QY 21 ValThrIleLeuLeuLeuValAlaIleAlaGlyAsnGlyPheIleThrAla 40
Db 28 GTTGTGCTTTAGCTGTGATGCTTTCGGGATGTCAGCAATGGCTTCTATGTCGTG 87
QY 41 AlaLeuGlyValAlaGluTrpValLeuArgArgMetLeuLeuProCysAspIlyLeuVal 60
Db 88 GTGCTGGCAGGAGGTGCTGCAATGTCAGAGTTGCTCCCTTGATGTGATCCCAT 147
QY 61 SerLeuGlyAlaSerArgPheCysLeuGlnSerValValMetGlyIlyThrIleTyVal 80
Db 148 AGCTTGGGTGCTCCCGCTTCTGCTGCAAGTTGGTGGACGGTCACAACTTCTATC 207
QY 81 PheLeuHisProMetAlaPheProTyArgProValLeuGlnPheLeuAlaPheGlnTrp 100
Db 208 TGTGCCAGAAAGTGCAGTACTGTGGGGTCTCGGCCGACAGTTTCCATCTACACTGG 267
QY 101 AspPheLeuLeuAlaAlaThrLeuTrpSerSerThrTrpLeuSerValPheTyArgVal 120
Db 268 CACTTCTGATACCTCACACCACTTCTGCTTTCAGAGTGGCTGAGTCTGCTGTG 327
QY 121 LysIleAlaThrPheThrHisProValPhePheTrpLeuIlyHisIlyLeuSerGlyTrp 140
Db 328 AGATTTGCTAACATCAACACTCCACCTTCTGCTGCTAAGTGAAGTCCAGAGGTGG 387
QY 141 LeuProTrpMetLeuPheSerSerValGlyLeuSerSerPheThrThrIleLeuPhePhe 160
Db 388 GTGCCCTGGCTGCTGTGGGCTGTGCTGATCTCTTCATCATAACTCGCTGTTTTT 447
QY 161 IleGlyAspHisArgMetTyArgIleuTrpLeu-----ArgAsnHisLeu 175
Db 448 TGGGTAACTACCTGATATCAAGAAATTTTAATTAAGAAATTTTCTGGAAACATGACC 507
QY 176 GlnProTrpAsnValThrGlyAspSerIleArgSerTyCysGlyIlyAspPheTyLeuPhe 195
Db 508 TACAACTGGAAT-----ACAAAGATGAAGAACATACATATTTTCCCA 546
QY 196 ProLeuIlyMetIleThrTrpThrMetProThrAlaValPhePheIleCysMetIleLeu 215
```



GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: February 4, 2005, 19:59:28 / Search time 3688 Seconds  
(without alignments)  
3282.114 Million cell updates/sec

Title: US-10-628-464-2

Perfect score: 1678  
Sequence: 1 MNDGHWLVSSVTDKXAIL.....SNCRLRAVLKSRSSRCGTP 318

Scoring table:  
BLOSUM62  
Xgapop 10.0, Xgapext 0.5  
Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
-MODEL=frame+g2n.model -DEV=xlh  
-O=/cgr2\_1/USPTO.spool/US10628464/runat\_04022005\_115948\_4337/app\_query.fasta\_1.455  
-DB=EST -OPMT=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOFCU=0 -LOOPEXT=0  
-UNITS=bites -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-LOCALIGN=200 -THR\_SCORE=pcr -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=pcr -NOR=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000  
-USR=US10628464\_@CGN\_1\_1\_4352\_@runat\_04022005\_115948\_4337 -NCPU=6 -ICPU=3  
-NO\_MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -MAIN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database:

EST: \*  
1: gb\_estc1: \*  
2: gb\_estc2: \*  
3: gb\_hic: \*  
4: gb\_estc3: \*  
5: gb\_estc4: \*  
6: gb\_estc5: \*  
7: gb\_estc6: \*  
8: gb\_gss1: \*  
9: gb\_gss2: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	345	20.6	893	9	AY403663 Pan trogl
2	336	20.0	900	9	AY403662 Homo sapi
3	326	19.4	894	9	AY403664 Mus muscu
4	321.5	19.2	866	7	CN840760 AGENCOURT
5	307.5	18.3	717	7	CF147792 AGENCOURT
6	297.5	17.7	771	9	CC544773 CH240_427
7	293	17.5	806	4	BG209561 RST29087
8	286.5	17.1	895	7	CN839536 AGENCOURT
9	284	16.9	650	8	AQ316999 CITBI-E1-

10	284	16.9	742	8	AQ308694
C 11	284	16.9	787	8	AZ739176
C 12	283	16.9	850	7	CN835406
C 13	262	15.6	917	7	CN842886
C 14	254.5	15.2	851	9	CC521365
C 15	246.5	14.7	883	7	CN836429
C 16	245.5	14.6	894	9	AY404528
C 17	235	14.0	715	7	CF147795
C 18	234	13.9	700	8	BH265706
C 19	232	13.8	530	9	CE673154
C 20	232	13.8	913	7	CN843081
C 21	228	13.5	2418	3	AF116728
C 22	227	13.5	493	8	BZ898478
C 23	221.5	13.2	870	9	CR071716
C 24	214	12.8	718	7	CF147794
C 25	211.5	12.6	884	7	CN839562
C 26	210	12.5	921	7	CN843110
C 27	207	12.3	758	4	BG203110
C 28	207	12.3	853	7	CN839414
C 29	206.5	12.3	921	7	CN835918
C 30	204.5	12.2	744	7	CO935442
C 31	204	12.2	737	7	CO960534
C 32	201.5	12.0	639	8	BZ922748
C 33	199.5	11.9	852	7	CN835976
C 34	198.5	11.8	900	9	AY404526
C 35	196	11.7	414	8	BH614820
C 36	193	11.5	741	9	AG374557
C 37	191.5	11.4	871	7	CN835432
C 38	191	11.4	711	7	CF147793
C 39	191	11.4	711	7	CO926496
C 40	189.5	11.3	699	8	BZ604233
C 41	183.5	10.9	947	7	CN838521
C 42	182.5	10.9	528	8	BH044856
C 43	182.5	10.9	804	7	CN841612
C 44	177.5	10.6	885	7	CN836251
C 45	176	10.5	681	9	CE066229

#### ALIGNMENTS

RESULT 1	AY403663	893 bp	DNA	linear	GSS 15-DEC-2003
LOCUS	AY403663				
DEFINITION	Pan troglodytes TMS2R1 gene, VIRTUAL TRANSCRIPT, partial sequence.				
ACCESSION	AY403663				
VERSION	AY403663.1	GI:39759646			
KEYWORDS	GSS.				
SOURCE	Pan troglodytes (chimpanzee)				
ORGANISM	Pan troglodytes				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.				
AUTHORS	1 (bases 1 to 893) Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Clevello,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Snihsy,J.J., Rietler,S., Wang,G., Zheng,X.H., White,T.J., Snihsy,J.J., Adams,M.D. and Cargill,M.				
TITLE	Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios				
JOURNAL	Science 302 (5652), 1960-1963 (2003)				
REFERENCE	PUBMED 14671302				
AUTHORS	2 (bases 1 to 893) Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Clevello,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Snihsy,J.J., Adams,M.D. and Cargill,M.				
TITLE	Direct Submission				
JOURNAL	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA				
COMMENT	This sequence was made by sequencing genomic exons and ordering them based on alignment.				
FEATURES	Location/Qualifiers				
SOURCE	1. .893				

